

STIC-Biotech/ChemLib

67938

From: Bunner, Bridget
Sent: Tuesday, June 04, 2002 8:47 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like the following sequence searched for case 09/655,272:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailroom 10C01

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

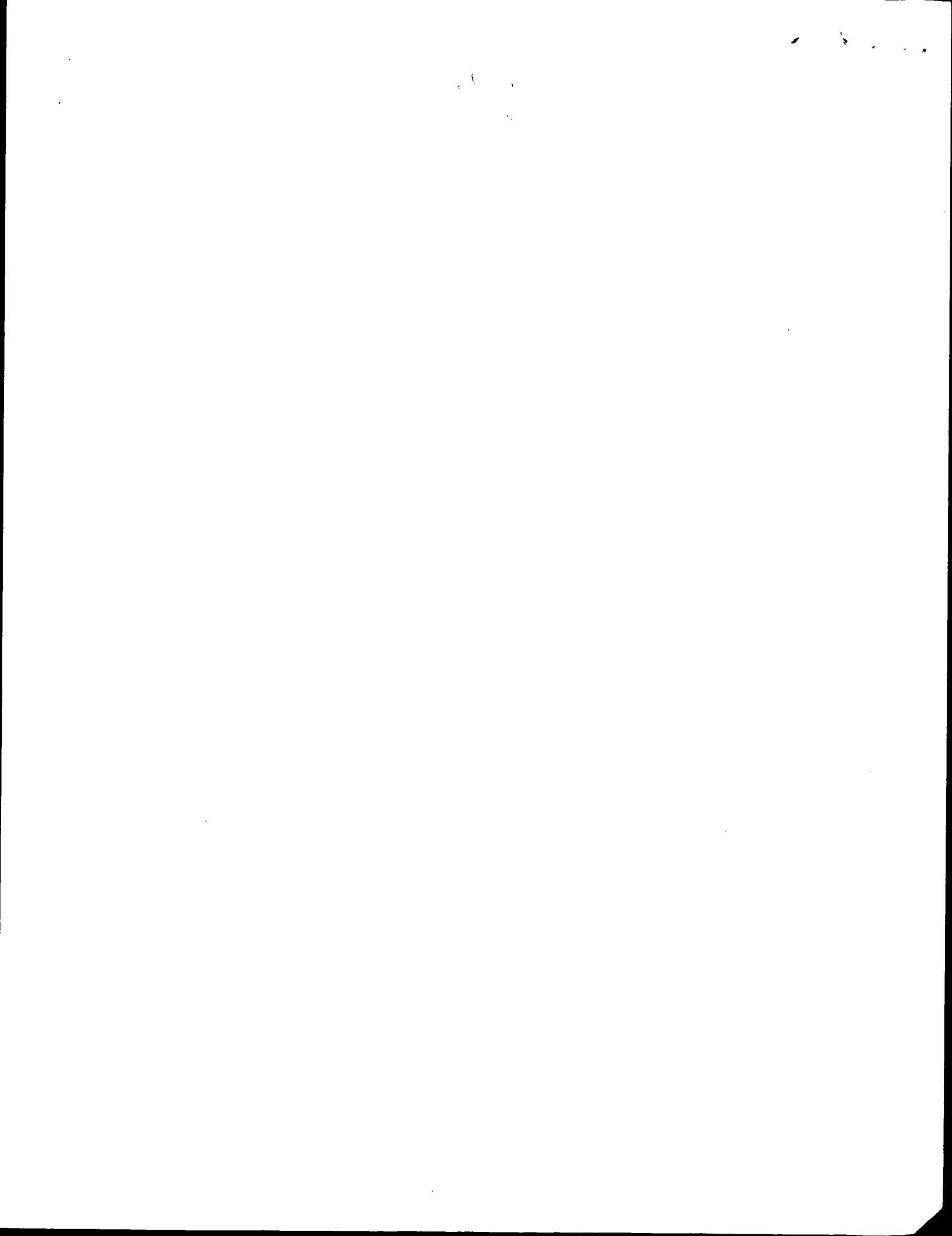
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/4/02
Date Completed: 6/4/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1 _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02 _____
WWW/Internet: _____
Other (specify): _____



Tue Jun 4 11:44:27 2002

us-09-655-272-2.rsP

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 4, 2002, 11:00:16 ; Search time 13.41 seconds
(without alignments)
1149.171 Million cell updates/sec

Title: US-09-655-272-2
Perfect score: 2079
Sequence: 1 MRSSTLLALLLVLLVLSG.....SKKSPRGRGLRDKAVPV 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SWISSPROT_40:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match Length	ID	Description
1	2079	100.0	C1W4_MOUSE	088454 mus musculu
2	1692.5	81.4	C1W4_HUMAN	094978 homo sapien
3	790	38.0	C1W4_HUMAN	P57789 homo sapien
4	788	37.9	C1W4_RAT	091354 rattus norv
5	770.5	37.1	C1W2_MOUSE	P97438 mus musculu
6	759.5	36.5	C1W2_HUMAN	095069 homo sapien
7	416	20.0	C1W6_HUMAN	095279 homo sapien
8	386	18.6	C1W1_HUMAN	000180 homo sapien
9	379.5	18.3	C1W1_MOUSE	008581 mus musculu
10	369.5	17.8	C1W1_MOUSE	094526 dirosophila
11	353	17.0	C1W1_MOUSE	091158 cavia porce
12	333.5	16.0	C1W3_MOUSE	031111 mus musculu
13	332.5	16.0	C1W3_MOUSE	054912 rattus norv
14	332.5	16.0	C1W3_MOUSE	094922 homo sapien
15	327.5	15.8	C1W3_MOUSE	014649 mus musculu
16	326.5	15.7	C1W3_MOUSE	094221 mus musculu
17	282.5	13.6	C1W7_MOUSE	094202 homo sapien
18	260	12.5	C1W7_MOUSE	P34410 caenorhabdi
19	216.5	10.4	C1W7_MOUSE	P40310 saccharomyc
20	168.5	8.1	C1W7_MOUSE	P17600 homo sapien
21	132	6.3	C1W7_MOUSE	P17600 homo sapien
22	131	6.3	C1W7_MOUSE	P17600 homo sapien
23	130	6.3	C1W7_MOUSE	P17600 homo sapien
24	129	6.2	C1W7_MOUSE	P17600 homo sapien
25	125	6.0	C1W7_MOUSE	P17600 homo sapien
26	124	6.0	C1W7_MOUSE	P17600 homo sapien
27	123.5	5.9	C1W7_MOUSE	P17600 homo sapien
28	121	5.8	C1W7_MOUSE	P17600 homo sapien
29	120.5	5.8	C1W7_MOUSE	P17600 homo sapien
30	118	5.7	C1W7_MOUSE	P17600 homo sapien
31	115.5	5.6	C1W7_MOUSE	P17600 homo sapien
32	114.5	5.5	C1W7_MOUSE	P17600 homo sapien
33	114	5.5	C1W7_MOUSE	P17600 homo sapien

RESULT	1	ALIGNMENTS
ID	C1W4_MOUSE	STANDARD: PRT; 398 AA.
AC	088454	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Potassium channel subfamily K member 4 (TWIK-related arachidonic acid- stimulated potassium channel protein) (TRAAK).	
DE	stimulated potassium channel protein (TRAAK).	
DE	KCNK4 OR TRAAK.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
CC	NCBI-TaxID=10090;	
OX	[1]	
RP	SEQUENCE FROM N.A.	
RP	TISSUE=Brain;	
RC	MEDLINE=98292450; PubMed=9628867;	
RX	Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M., Lazdunski M.;	
RA	"A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids."	
RT	EMBO J. 17:3297-3308(1998).	
RL	[2]	
RL	ACTIVATION: 99254548; PubMed=10321245;	
RP	MEDLINE=99254548; PubMed=10321245;	
RX	Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.,	
RA	"Inhalational anesthetics activate two-pore-domain background K+ channels."	
RT	Neurosci. 2:422-426(1999).	
RL	NET. FUNCTION: VOLTAGE-SENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH POTASSIUM K+ CONCENTRATIONS.	
CC	EXTERNAL K+ CONCENTRATIONS.	
CC	-1- SUBUNIT: HOMODIMER (POTENTIAL).	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (potential).	
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND	
CC	2/TRAFFIC/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.	
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE, NOT	
CC	DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND	
CC	TESTIS.	
CC	-1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED	
CC	FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANESTHETICS SUCH AS	
CC	CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.	
CC	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM	
CC	CHANNELS.	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation on	
CC	the European Bioinformatics Institute. There are no restrictions on its	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@sib-sib.ch).	
CC	EMBL; AF056492; AAC40181.1;	
DR	MCD; MG1:1298234; Kcnk4.	

DR InterPro: IPR003280; 2porek channel.
 DR InterPro: IPR000636; Cation_chan_non_1lg.
 DR Pfam: PF00520; Ion_trans_1.
 DR PRINTS: PR01333; 2POREKCHANEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 FT DOMAIN: Alternative splicing.
 FT TRANSMEM 1 3 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 89 113 PORE-FORMING 1 (POTENTIAL).
 FT TRANSMEM 119 139 POTENTIAL.
 FT TRANSMEM 140 171 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 198 222 PORE-FORMING 2 (POTENTIAL).
 FT TRANSMEM 235 255 POTENTIAL.
 FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 81 81 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 63 67 KLIVE -> KAMAI (IN ISOFORM 2).
 FT VARSPLIC 68 398 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 398 AA; 43051 MW; 476834B7B7EC92 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 2079; DB 1; Length 398;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR 1 MRSTTLALALVLLVYSGALVFOALPOHPOHQAOKKMDHGRDQFLRDPVCSOKSLD 60
 DB 1 MRSTTLALALVLLVYSGALVFOALPOHPOHQAOKKMDHGRDQFLRDPVCSOKSLD 60
 QY 61 FIKLVEALGGANPEWTNSSHSSAMNLSGSAFFSGTITITIGYGNVLTHTDAGRLF 60
 DB 61 FIKLVEALGGANPEWTNSSHSSAMNLSGSAFFSGTITITIGYGNVLTHTDAGRLF 120
 QY 121 CIEFALVGIPLFGMLLAGVDRGSSLRIGIHEIAIFLKHVPGLVNSLSAVFLILG 120
 DB 121 CIEFALVGIPLFGMLLAGVDRGSSLRIGIHEIAIFLKHVPGLVNSLSAVFLILG 180
 QY 181 CLFVLPTPEVFSYMSKSLFAIVYVLTGFGDVPDGGTGSNSPAYOPLVWFMI 180
 DB 181 CLFVLPTPEVFSYMSKSLFAIVYVLTGFGDVPDGGTGSNSPAYOPLVWFMI 240
 QY 241 LFGIAPVAVLTITIGMWLRAVSRRTRAEMGGLTAAASWTGTVAARYORTGSPAPPEK 240
 DB 241 LFGIAPVAVLTITIGMWLRAVSRRTRAEMGGLTAAASWTGTVAARYORTGSPAPPEK 300
 QY 301 EOPILPSSLPAPPAVEPAGRGSPAPAEKVEPSPPTASALDYPSENLAFFIDESSDTOS 300
 DB 301 EOPILPSSLPAPPAVEPAGRGSPAPAEKVEPSPPTASALDYPSENLAFFIDESSDTOS 360
 QY 361 ERGICALPAPRRRRPNSSKSPRRPGRLRDKAVPV 398
 DB 361 ERGICALPAPRRRRPNSSKSPRRPGRLRDKAVPV 398

RESULT 2
 C1W4_HUMAN STANDARD; PRT; 393 AA.
 AC Q2NYG8;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DE 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Stimulated channel subfamily K member 4 (TWIK-related arachidonic acid-
 GN KCNK4 OR TRAAK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RA MEDLINE=20499203; PubMed=11042359;
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
 RA Keisell R.E., Murdoch P.R., Randall A.D., Renne G.I., Glover I.S.;
 RT "Cloning, localisation and functional expression of a novel human,
 RT cerebellum specific, two pore domain potassium channel.";
 RL Brain Res. Mol. Brain Res. 82:74-83(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Frontal cortex;
 RA Gray A.T.;
 RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
 RT chromosome 11.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20231699; PubMed=10767409;
 RA Lesage F., Maignret F., Lazdunski M.;
 RT "Cloning and expression of human TRAAK, a polyunsaturated fatty
 RT acids-activated and mechano-sensitive K(+) channel.";
 RL FEBS Lett. 471:137-140(2000).
 CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
 CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.

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 CC EMBL; AF248242; AAC31731.1; -
 CC MIM; 605720; -
 CC DR EMBL; AF247042; AAF64062.1; ALT_INIT.

DR InterPro: IPR003280; 2porek channel.
 DR InterPro: IPR000636; Cation_chan_non_1lg.
 DR InterPro: IPR001622; Channel_pore_K.
 DR Pfam: PF00520; Ion_trans_1.
 DR PRINTS: PR01333; 2POREKCHANEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
 FT DOMAIN: Alternative splicing.
 FT TRANSMEM 1 3 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 89 113 PORE-FORMING 1 (POTENTIAL).
 FT TRANSMEM 118 138 POTENTIAL.
 FT TRANSMEM 140 171 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 197 221 PORE-FORMING 2 (POTENTIAL).
 FT TRANSMEM 221 254 POTENTIAL.
 FT TRANSMEM 235 255 POTENTIAL.
 FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 78 78 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 328 328 P -> L (IN REF. 2).
 SQ SEQUENCE 393 AA; 42704 MW; 7F18E35A09AD57D CRC64;

Query Match
 Best Local Similarity 81.4%; Score 1692.5; DB 1; Length 393;
 Matches 328; Conservative 24; Mismatches 41; Indels 5; Gaps 2;

DR 1 MRSTTLALALVLLVYSGALVFOALPOHPOHQAOKKMDHGRDQFLRDPVCSOKSLD 60
 DB 1 MRSTTLALALVLLVYSGALVFOALPOHPOHQAOKKMDHGRDQFLRDPVCSOKSLD 60
 QY 61 FIKLVEALGGANPEWTNSSHSSAMNLSGSAFFSGTITITIGYGNVLTHTDAGRLF 120
 DB 61 FIKLVEALGGANPEWTNSSHSSAMNLSGSAFFSGTITITIGYGNVLTHTDAGRLF 120


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Query Match      37.1%; Score 770.5; DB 1; Length 411;
Best Local Similarity 49.8%; Pred. No. 5.4e-35;
Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1.

OY      1 MRSSTLLALALVLLVYSGALVFQALQPHQQAOKMKDHGRQFLIRHPCVQSQSLD 60
| : | : : : | : | : | : | : | : | : | : | : | : | : | : | : | :

```

Db 42 MKKTVSTFLVVLVLLIGAAVEKALEOPDISQRTIVIOKQFIAGHACVNSTELDE 101
QY 61 FIKLVEALGGANPETSWTNSNHSANWLGSAFFSGTITITIGCNVLTHTDAGRLF 120
Db 102 LIQOIVAAIMAGIIP---LGNSNOYSHWDLGSSFFFACTVITITIGFINSPTREGKIF 158
QY 121 CIFVALVGIPLFEGMLLAGVDRGLSSLRGIGHEAIFLKWHPGGLVRSLSAVFLILIG 180
Db 159 CIIVALLGIPLEFGLLAGVQDGLTIFGKIAKVEDTPIKMNVSQTKIRIISTIFILFG 218
QY 181 CLLEFLVLPFVFESYMSKLEAIFVIVLTITVFGDYVPGDGTGNSPAYOPLVFWMI 240
Db 219 CVLFLVLPVAFVIFKHIEGMSALDAIFVIVLTITVFGDYVAGSDIEYDFKPVVFWMI 278
QY 241 LFLGAFVASYLTITIGNMLRAVSRRTAEKGGTLQAASWTGVTYA 285
Db 279 LVGLAFVAVLSMIGMLRVISKTKKEVGERRAHAEMTANYTA 323

RESULT 6
C1W2_HUMAN STANDARD: PRT: 426 AA.
AC 095069; O9UNE3; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore potassium channel TRPK1).
GN KCNK2 OR TREK1 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=99354548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+ channels".
RT Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price E.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RT Submitted (May-1997) to the EMBL/Genbank/DBS databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC -----
CC EMBL: AF129399; AAD47569.1; -;
CC EMBL: AF004711; AAD01203.1; -;
CC MIM: 603219; -;
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR003976; Trek_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PRO1333; 2PORECHANEL.
DR PRINTS: PRO1499; TREKCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KW Glycoprotein. 1 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 62 82 POTENTIAL.
FT TRANSMEM 144 170 PORE-FORMING 1 (POTENTIAL).
FT DOMAIN 172 192 POTENTIAL.
FT TRANSMEM 173 223 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 224 244 POTENTIAL.
FT TRANSMEM 253 283 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 308 308 POTENTIAL.
FT DOMAIN 378 426 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 354 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
FT DOMAIN REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).
FT CARBOHD 110 110 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHD 134 134 N-LINKED (GLCNAc...) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009FAE CRC64;

Query Match 36.5%; Score 759.5; DB 1; Length 426;
Best Local Similarity 49.1%; Pred. No. 2.2e-34;
Matches 140; Conservative 57; Mismatches 85; Indels 3; Gaps 1;

QY 1 MRSTLLALLALVLYVSGALVFOALQPHEDQAOKMDHGRDFLDRHCYSQKSLSD 60
Db 57 MKKTVSTFLVVLVLLIGAAVEKALEOPDISQRTIVIOKQFIAGHACVNSTELDE 116
QY 61 FIKLVEALGGANPETSWTNSNHSANWLGSAFFSGTITITIGCNVLTHTDAGRLF 120
Db 117 LIQOIVAAIMAGIIP---LGNSNOYSHWDLGSSFFFACTVITITIGFINSPTREGKIF 173
QY 121 CIFVALVGIPLFEGMLLAGVDRGLSSLRGIGHEAIFLKWHPGGLVRSLSAVFLILIG 180
Db 174 CIIVALLGIPLEFGLLAGVQDGLTIFGKIAKVEDTPIKMNVSQTKIRIISTIFILFG 233
QY 181 CLLEFLVLPFVFESYMSKLEAIFVIVLTITVFGDYVPGDGTGNSPAYOPLVFWMI 240
Db 234 CVLFLVLPVAFVIFKHIEGMSALDAIFVIVLTITVFGDYVAGSDIEYDFKPVVFWMI 293
QY 241 LFLGAFVASYLTITIGNMLRAVSRRTAEKGGTLQAASWTGVTYA 285
Db 294 LVGLAFVAVLSMIGMLRVISKTKKEVGERRAHAEMTANYTA 338

RESULT 7
C1W5_HUMAN STANDARD: PRT: 499 AA.
AC 095279; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).
GN KCNK5 OR TASK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99030343; PubMed=9812978;
RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N., Lazdunski M.;
RT "Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney".
RT J. Biol. Chem. 273:30863-30869(1998).
CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL

DR EMBL: AF281302; AAG10506.1; -
 DR EMBL: AF281303; AAG10507.1; -
 DR MIM: 603939; -
 DR InterPro: IPR000636; Cation_chan_non_11g.
 DR InterPro: IPR001622; Channel_pore_K.
 DR InterPro: IPR001779; TWIK1_channel.
 DR Pfam: PF00520; Ion_trans. 1.
 DR PRINTS: PR01096; TWIK1CHANNEL.
 DR Ionic channel: Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein; Alternative splicing.
 FT DOMAIN 1 4
 FT TRANSMEM 5 25
 FT DOMAIN 90 115
 FT TRANSMEM 121 141
 FT DOMAIN 142 172
 FT TRANSMEM 173 193
 FT DOMAIN 199 223
 FT TRANSMEM 236 256
 FT DOMAIN 257 313
 FT CARBOHYD 79 79
 FT CARBOHYD 85 85
 FT VARSPPLIC 1 134
 FT MOTAGEN 53 53
 FT SEQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;

Query Match 18.6%; Score 386; DB 1; Length 313;
 Best Local Similarity 34.8%; Pred. No. 1.8e-14;
 Matches 111; Conservative 51; Mismatches 131; Indels 26; Gaps 10;

QY 1 MRSTLLA-LTALVLYSGALVQALPEQHEQQAQKMDHGRDQFLRHPVCSQSKLE 59
 DB 1 MRGALLAGLAAALAAALVGLALVRLLEGPHRLRALETLRAQLQSPCAAPALD 60
 QY 60 DFILVLEALGGANPEFTSWTNSNHS-AMNLSAFPSGTTITTYGYNIVLHNDAGR 118
 DB 61 AFVERVLAAGLGRVLANASGSANASDPAMDFAALFSTLTITTYGYTPPLTDAGK 120
 QY 119 LFCIFYALVIGIFEGMLLAGVGRIGSLRRGIGHIEAIFL-KWHVPGLVRSLSAVLF 176
 DB 121 AFSTAFALVGPVTMLLTASQRLSLTLT-HVPLSWLSMGWMDPR--RAACWHLV 174
 QY 177 LLIGCLFV--LTPEFVSYS-ESMSKLEATYFIVLTITGFGDYGSGDGTGNSPA-Y 232
 DB 175 ALIGVAVVCELVPAVVFPAHLEAMSEFDATYFCFISTIGLGDYVGEARQPYRALY 234
 QY 233 QPLVFWILFGLAFASVLTITGNMLRAVSRRTAEMGLT--AQAASWTGTVTARYTQ 289
 DB 235 KVLVAVVLEGLVAMVVLQTF-----RHVSDHLGLTLLPPLPCPASFNADDD 285
 QY 290 RTGPSAPPEKEQPLPSS 308
 DB 286 RVDILGPOPESHQOLSSASS 304

RESULT 9
 C1WL_HUMAN STANDARD; PRT; 336 AA.
 AC 000180; Q13307;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium channel subfamily k member 1 (Inward rectifying potassium
 channel protein TWIK-1) (Potassium channel KCNK1).
 GN KCNK1 OR TWIK1 OR HOK1 OR KCNK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
 RC TISSUE=Kidney;
 RX MEDLINE=96183184; PubMed=8605869;

RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
 RA Barhanin J.,
 RA "TWIK-1, a ubiquitous human weakly inward rectifying K⁺ channel with a
 RA novel structure.";
 RL EMBO J. 15:1004-1011(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND REVIEW.
 RC TISSUE=Brain;
 RX MEDLINE=96122696; PubMed=9462864;
 RA Goldstein S.A.N., Wang K.W., Ilian N., Pausch M.H.;
 RA "Sequence and function of the two P domain potassium channels:
 RA implications of an emerging superfamily.";
 RL J. Mol. Med. 76:13-20(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96026667; PubMed=9362344;
 RA Orlas M., Velazquez H., Tung F., Lee G., Desir G.V.;
 RA "Cloning and localization of a double-pore K channel, KCNK1: exclusive
 RA expression in distal nephron segments.";
 RL Am. J. Physiol. 273:F663-F666(1997).
 CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
 CC BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
 CC INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC -----
 DR EMBL: U33632; AAB01688.1; -
 DR EMBL: U76996; AAB97878.1; -
 DR EMBL: U90065; AAB51147.1; -
 DR MIM: 601745; -
 DR InterPro: IPR003280; 2porek_channel.
 DR InterPro: IPR000636; Cation_chan_non_11g.
 DR InterPro: IPR001622; Channel_pore_K.
 DR InterPro: IPR001779; TWIK1_channel.
 DR Pfam: PF00520; Ion_trans. 1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR PRINTS: PR01096; TWIK1CHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 20
 FT TRANSMEM 21 41
 FT DOMAIN 104 130
 FT TRANSMEM 133 153
 FT DOMAIN 154 177
 FT TRANSMEM 178 198
 FT DOMAIN 212 238
 FT TRANSMEM 247 267
 FT DOMAIN 268 336
 FT CARBOHYD 95 95
 FT MOTAGEN 161 161
 FT SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;

Query Match 18.3%; Score 379.5; DB 1; Length 336;
 Best Local Similarity 34.4%; Pred. No. 4.2e-14;
 Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;
 QY 2 RSTLLALLA-LVLYVSGALVQALPEQHEQQAQKMDHGRDQFLRHPVCSQSKLE 60
 DB 18 RSMCFGVLVGLYLLVFGAVVSSVLPYEDLLRQELRKRLKRFLEHCHLSQQLQ 77

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QY 61 FIKLVEALGG---ANPETSNTSSNHSANLGSAPFPGTITTTIGNVLHTTA 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 FLGRVLEALNAGVSVLSNAGNMN-----WDFTSALFFASTVSTTGTVPLSDG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 GRFCIEFYALVGIPLFGMLLAGVGRDGLSSL-RRGIGHIEALFKWHPGLVRSLSAVL 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 GKAFCLITVSVIGPFTLLFTAVQRTVHVRRLVYFH---IRMGFSKQVAVIHAVL 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 -FLIGCLLEFLVPTFVSYSME-SMSKLEAIFYVITLTGFGDYGVDGTGQN-SPA 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 LGEFVVSCEFFI--PAAVSVLEDDMNLFESYFCFISLTIGLGDYVPEGYNOKFREL 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 YQPLVWFVWLEFLAIFYASVLT 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 YKIGTCYLLGLLIMLVLET 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
C1W1_MOUSE STANDARD: PRT: 336 AA.
AC 008581:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 1 (Inward rectifying potassium
   channel protein TWIK-1).
GN KCNK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97165959; PubMed=9013852;
RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
   Lqadunski M.;
RT "The structure, function and distribution of the mouse TWIK-1 K+
   channel";
RL FEBS Lett. 402:28-32(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RX MEDLINE=98218573; PubMed=9559671;
RA Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;
RT "Structure, chromosome localization, and tissue distribution of the
   mouse twik K+ channel gene";
RL FEBS Lett. 425:310-316(1998).
RN [3]
RP FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -SUBUNIT: HOMODIMER (POTENTIAL).
CC -SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
   KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
   EPIDIDYMIS, UTERUS, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
   OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
   MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
   CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
   CORTEX.
CC -DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
   CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
   STABILIZES AFTER DAY 8.
CC -MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
   ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
   CHANNELS.
CC -----
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CC -----
CC EMBL: AF033017; AAC16973.1; -
DR MGD: MGI:109322; Kcck1.
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_1ig.
DR InterPro: IPR001622; Channel_pore_k.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PRO133; 2PORECHANNEL.
DR PRINTS: PRO1096; TWIK1CHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;

Query Match 17.8%; Score 369.5; DB 1; Length 336;
Best Local Similarity 34.0%; Pred. No. 1.4e-13;
Matches 89; Conservative 53; Mismatches 97; Indels 23; Gaps 9;

QY 2 RSTLLALAL-VLTVLSGALFQALQPHQQAQRKRDGDFLRDHPVQSOKSLSD 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 RSMWCFGLVLTGLTVGAVFSSSELPYEDLRKLRRLRREHCLSEPOLEQ 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 FIKLVEALGG---ANPETSNTSSNHSANLGSAPFPGTITTTIGNVLHTTA 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 FLGRVLEALNAGVSVLSNAGNMN-----WDFTSALFFASTVSTTGTVPLSDG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 GRFCIEFYALVGIPLFGMLLAGVGRDGLSSL-RRGIGHIEALFKWHPGLVRSLSAVL 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 GKAFCLITVSVIGPFTLLFTAVQRTVHVRRLVYFH---IRMGFSKQVAVIHAVL 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 -FLIGCLLEFLVPTFVSYSME-SMSKLEAIFYVITLTGFGDYGVDGTGQN-SPA 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 LGEFVVSCEFFI--PAAVSVLEDDMNLFESYFCFISLTIGLGDYVPEGYNOKFREL 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 YQPLVWFVWLEFLAIFYASVLT 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 YKIGTCYLLGLLIMLVLET 266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
ORF1_DROME STANDARD: PRT: 1001 AA.
AC 094526:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Open rectifier potassium channel protein 1 (Two pore domain potassium
   channel ORK1).
GN ORK1 OR CG1615.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larva;
RX MEDLINE=97075152; PubMed=8917578;
RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.;
RT "ORK1, a potassium-selective leak channel with two pore domains
   cloned from Drosophila melanogaster by expression in Saccharomyces

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FT	DOMAIN	1	6	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	7	27	POTENTIAL.
FT	DOMAIN	95	111	PORE-FORMING 1 (POTENTIAL).
FT	TRANSMEM	120	140	POTENTIAL.
FT	DOMAIN	141	170	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	171	191	POTENTIAL.
FT	DOMAIN	208	224	PORE-FORMING 2 (POTENTIAL).
FT	TRANSMEM	244	264	POTENTIAL.
FT	DOMAIN	265	1001	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	58	58	N-LINKED (GLCNAC. .) (POTENTIAL).
SO	SEQUENCE	1001 AA;	109289 MW;	09AE1A369072E07 CRC64;
Query Match		17.0%;	Score 353;	DB 1; Length 1001;
Best Local Similarity		29.1%;	Pred. No. 3.1e-12;	
Matches		95;	Conservative 54;	Mismatches 104; Indels 74; Gaps 9;
OY	7 LALLALVLLIVSGLVAVQALEOPHEHOQAOKKMDHGRQFLPDHCVCOKSLIEDPIKLIV	66		
Db	7 ILLLFYSIYLMEFAIIYYHIE-----HGEEKISRAEQRKQAIANEY--LL	51		
OY	67 EALGG-----ANPETSWTNSNHSAMNGSAFFGFGITTTGYCNI	110		
Db	52 BELGKNNTTODEILLQRISDCDKRVTLTPPTDDPYTWTFYTHAFEFYFCSTGVGNI	111		
OY	111 VLHTDAGRILFCIFVALVGIPLFEGMLLAGVDRLGSSLRIGIHTEAIPLKK-----	161		
Db	112 SPPTFAGMIMIAVSIGIVPGVLFPAGLGGEYFGRT-----PEAIRRYRKYKMSIDM	164		
OY	162 -HVPPGLVRSLSAVLPFLIGCLLEPVLTPEFVSYESKSKEALFYVTLTVGFGGIV	220		
Db	165 HYPVPLLITTYVTALPGIALFLLPSWVFYEENMPYSLSLYSVYTTTTTGFDYV	224		
OY	221 PDGDGQNSP-----AYOPLWFMLEGLAFASVLTTIGMWLAARYSRTRAEKGTLTA	274		
Db	225 PTFGNQKEREGMGVVYQIFYIWMFIFTSIGLVLMFMFITRGLOS-----KLATYLEQ	278		
OY	275 QAAS-----WTGTVAITYORTQG	292		
Db	279 QLSMLKATQNRMISG-----VTKDVG	300		
RESULT	12			
ID	CIW9_CAVPO	STANDARD;	PRT;	365 AA.
AC	09JUL58:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3). KCNK9 OR TASK3.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
OX	NCBI_TaxId=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	Medline=20287530; PubMed=10747866;			
RA	Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,			
RA	Karschin A., Derst C.;			
RT	"TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An			
RT	extracellular histidine as pH sensor."			
RL	J. Biol. Chem. 275:16650-16657(2000).			
CC	-1 FUNCTION: PH-DEPENDENT VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN.			
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1 SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.			
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 CC -----
 DR EMBL: AF212827; AAF63706.1; -
 DR InterPro: IPR003280; 2porek_channel.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001622; Channel_pore_K.
 DR InterPro: IPR003092; TASK_channel.
 DR Pfam: PF00520; Ion_trans.1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR PRINTS: PR01095; TASKCHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KM Glycoprotein.
 FT DOMAIN 1 8
 FT TRANSMEM 9 29
 FT DOMAIN 78 101
 FT TRANSMEM 108 128
 FT DOMAIN 129 158
 FT TRANSMEM 159 179
 FT DOMAIN 184 207
 FT TRANSMEM 219 239
 FT DOMAIN 240 365
 FT CAROHYD 53 53
 SO SEQUENCE 365 AA; 40769 MW; 261DC973FE53AF91 CRC64;

Query Match 16.0%; Score 333.5; DB 1; Length 365;
 Best Local Similarity 28.3%; Pred. No. 1.3e-11;
 Matches 104; Conservative 55; Mismatches 124; Indels 85; Gaps 12;

QY 7 LALLALVLYVSGALVFOALBPHEQQAQKMDHGRDPLRHPVCSQR---SLEDFIK 63
 DB 9 LSLIACTFTYLLVGAALVPALESDHEHREKEL---KAERIR---IRKYNISTEDYRQ 61
 QY 64 LVEALGCGANPEPTWNTSSNNHSSA--WNLSAFPSGTTITIGYGNVILHTDAGRLFC 121
 DB 62 LELVIL-----QSPHRAGVQWKRKAGSFYFAITVITITIGYGNAPGTDAGARFC 110
 QY 122 IFYALVGLPLFGLMLAGVGRGLSLRIGIETALFLKWHVPPGLVRSLSAVLFLIGC 181
 DB 111 MEFAVGLIDPLTIVMFQSLGERMNTFVRLKRIKCCGMENTEVSMVTGVFFSCMG 170
 QY 182 LLEVLFTFEVSMESKLEATYIVLTITVYFGDYV--PDGTCQNSPAQPLVWFM 239
 DB 171 LCI---GAAAFSCQCEMSFPHAYVCTITLTITGFDYVALQSKGALQRRPFAVSFMY 227
 QY 240 ILFGLAYF-----ASVLTITIGMLRAVSRRT 266
 DB 228 ILVGLVIGAFMLVYLRFLTMSDSERGERGEGALPGNPSVYVHISEAQQVRRYR 287
 QY 267 AEMGGLTAQAASWTGVTARVORTGPS-----APPE-----KEOPLPLSSL-----P 310
 DB 288 GREGDILQ-----SVSCACYRSQPNFGATLAPQLPHISCRTEISPSLTKNSLFP 339
 QY 311 APPAYEP 318
 DB 340 SPISVSP 347

RESULT 13
 ID C1W3 MOUSE STANDARD; PRT; 409 AA.
 AC 035111; 035163;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium channel subfamily K member 3 (acid-sensitive potassium
 DE channel protein TASK) (TWIK-related acid-sensitive K+ channel)
 DE (Cardiac two-pore background K+ channel) (CTBAK-1).
 GN KCNK3 OR TASK OR CTBAK.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=98165556; PubMed=9506712;
 RT Kim D., Fujita A., Horio Y., Kurachi Y.;
 RT "Cloning and functional expression of a novel cardiac two-pore
 RT background K+ channel (CTBAK-1).";
 RL Circ. Res. 82:513-518(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=20287574; PubMed=10748056;
 RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
 RT "Proton block and voltage gating are potassium-dependent in the
 RT cardiac leak channel Kcnk3.";
 RL J. Biol. Chem. 275:16969-16978(2000).
 RN [3]
 RP SEQUENCE OF 4-409 FROM N.A.
 RX MEDLINE=97459932; PubMed=9312005;
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
 RT "TASK, a human background K+ channel to sense external pH variations
 RT near physiological pH.";
 RL EMBO J. 16:5464-5471(1997).
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
 CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
 CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
 CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
 CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
 CC IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
 CC INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
 CC -1- MISCELLANEOUS: INACTIVATED BY BARIUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
 CC -----
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 CC -----
 DR EMBL: AB008537; BAA25436.1; -
 DR EMBL: AF241798; AAF81418.1; -
 DR EMBL: AF242508; AAF81418.1; JOINED.
 DR EMBL: AF065162; AAG29339.1; -
 DR EMBL: AF006824; AAC53367.1; -
 DR EMBL: AB013345; BAA28349.1; -
 DR MGD: MGI:1100509; Kcnk3.
 DR InterPro: IPR003280; 2porek_channel.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR InterPro: IPR001622; Channel_pore_K.
 DR InterPro: IPR003092; TASK_channel.
 DR Pfam: PF00520; Ion_trans.1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR PRINTS: PR01095; TASKCHANNEL.
 KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 8
 FT TRANSMEM 9 29
 FT DOMAIN 78 101
 FT TRANSMEM 108 128
 FT DOMAIN 129 158
 FT TRANSMEM 159 179
 FT DOMAIN 184 207

FT TRANSMEM 223 243 POTENTIAL.
 FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 4 4 Q -> E (IN REF. 3).
 FT CONFLICT 123 123 V -> I (IN REF. 3).
 SO SEQUENCE 409 AA; 45068 MW; 35236E011AAC5687 CRC64;

Query Match 16.0%; Score 332.5; DB 1; Length 409;
 Best Local Similarity 31.6%; Pred. No. 1.7e-11;
 Matches 85; Conservative 44; Mismatches 97; Indels 43; Gaps 7;

QY 7 LALLALVILTVSGALVFPALQPHQQAOKKNDGRQFLRDHPCVSKSLIEDFKILLY 66
 DB 9 LALIVCTFTLLVGAVFALDSEPEMERQRLR-ROLELRARYNLSEGYEELERVL 67
 QY 67 EALGGANPETSWTNSNHSAMNLGSAFFSGTITITIGYNIYVLTADGRFCIFYAL 126
 DB 68 RLKPKHAGVQ-----WRFAGSYFAITVITITIGYHAPSDGKVFCEMFYAL 115
 QY 127 VGIPLEGMLAGVDRGLSSLR-----RGIG--HIEAIFLKMVHPGGLVRSLSAVLEL 177
 DB 116 LGIPPLTVMFQSLGERINTFVRYLLHRAKRGIGMRHAE-----VSMANVYLIG 163
 QY 178 LIGCLFLVLTPTFPVFSYMSKLEAIYFVITLTVGGDY--PGDGTGNSPAYQPL 235
 DB 164 FVSCISTLCIGAALFSTYERWTFQAYVYCFITLITIGFDYVALQKDALQTOPQY--- 220
 QY 236 VWFMIIFGLAFVAVSLTTIGNMLRAVSR 264
 DB 221 ----VAFSEFYIITGLTVIGAFNLVLYR 245

RESULT 14

CIM3_RAT
 ID CIM3_RAT STANDARD; PRT; 411 AA.
 AC 054912;
 DT 15-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K⁺ channel).
 GN KCKN3 OR TASK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RX MEDLINE=98099797; PubMed=9437008;
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
 RA "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum".
 RT J. Neurosci. 18:868-877(1998).
 RL J. Neurosci. 18:868-877(1998).
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.
 CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BOPIVACAIN AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

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 CC -----

DR EMBL: AF031384; AAC39952.1; -
 DR InterPro: IPR003280; 2poreK channel.
 DR InterPro: IPR000636; Cation_chan_non_119.
 DR InterPro: IPR001622; Channel_pore_K.
 DR InterPro: IPR003092; TASK_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR PRINTS: PR01333; 2PORECHANNEL.
 DR PRINTS: PR01095; TASKCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.
 KM
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 9 29 POTENTIAL.
 FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).
 FT TRANSMEM 108 128 POTENTIAL.
 FT TRANSMEM 129 158 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 159 179 POTENTIAL.
 FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
 FT TRANSMEM 223 243 POTENTIAL.
 FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 411 AA; 45276 MW; D278016B09E2B5 CRC64;

Query Match 16.0%; Score 332.5; DB 1; Length 411;
 Best Local Similarity 31.6%; Pred. No. 1.7e-11;
 Matches 85; Conservative 44; Mismatches 97; Indels 43; Gaps 7;

QY 7 LALLALVILTVSGALVFPALQPHQQAOKKNDGRQFLRDHPCVSKSLIEDFKILLY 66
 DB 9 LALIVCTFTLLVGAVFALDSEPEMERQRLR-ROLELRARYNLSEGYEELERVL 67
 QY 67 EALGGANPETSWTNSNHSAMNLGSAFFSGTITITIGYNIYVLTADGRFCIFYAL 126
 DB 68 RLKPKHAGVQ-----WRFAGSYFAITVITITIGYHAPSDGKVFCEMFYAL 115
 QY 127 VGIPLEGMLAGVDRGLSSLR-----RGIG--HIEAIFLKMVHPGGLVRSLSAVLEL 177
 DB 116 LGIPPLTVMFQSLGERINTFVRYLLHRAKRGIGMRHAE-----VSMANVYLIG 163
 QY 178 LIGCLFLVLTPTFPVFSYMSKLEAIYFVITLTVGGDY--PGDGTGNSPAYQPL 235
 DB 164 FVSCISTLCIGAALFSTYERWTFQAYVYCFITLITIGFDYVALQKDALQTOPQY--- 220
 QY 236 VWFMIIFGLAFVAVSLTTIGNMLRAVSR 264
 DB 221 ----VAFSEFYIITGLTVIGAFNLVLYR 245

RESULT 15
 CIM9_HUMAN
 ID CIM9_HUMAN STANDARD; PRT; 374 AA.
 AC 09NRC2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K⁺ channel 3).
 GN KCKN9 OR TASK3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20287530; PubMed=10747866;
 RA Rajan S., Mischmeyer E., Liu G.-X., Preisig-Mueller R., Daut J., Karschin A., Daut C.;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 4, 2002, 10:56:40 ; Search time 31.63 Seconds
(without alignments)
1397.641 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079

Sequence: 1 MRSSTLLALLLVLLVSG.....SKKRPSPGPGURKAVPV 398

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*

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20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*

21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2002.DAT:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2079	100.0	AAV30647	A mechanically sen
2	1692.5	81.4	AAV94425	Human h-TRAK poly
3	1692.5	81.4	AAV94426	Human h-TRAK poly
4	1692.5	81.4	AAV94426	Human h-TRAK poly
5	1688.5	81.2	AAV94571	Human G-protein co
6	895	43.0	AAV12229	Human K channel TR
7	776.5	37.3	AAV34133	Human potassium ch
8	776.5	37.3	AAV28496	h-TREK1 polypeptid
9	776.5	37.3	AAE10341	Human TREK-1 pote
10	776.5	37.3	AAE10341	Human TREK-1 pote
11	770.5	37.1	AAV30648	A mechanically sen

12	770.5	37.1	411	20	AAV28497	Mouse h-TREK1 poly
13	770.5	37.1	411	21	AAE10342	Murine TREK-1 pote
14	759.5	36.5	426	22	AAV07618	Human potassium io
15	755.5	36.3	426	22	AAV07622	Human potassium io
16	754.5	36.3	426	22	AAV07623	Human potassium io
17	753.5	36.2	426	22	AAV07624	Human potassium io
18	751.5	36.1	426	22	AAV07625	Human potassium io
19	427.5	20.6	332	22	AAE01027	Human TWIK-3 prote
20	427.5	20.6	332	22	AAE01027	Human TWIK-3 prote
21	416	20.0	499	21	AAV90356	Human TWIK-2 prote
22	416	20.0	499	21	AAV90356	Human TWIK-2 prote
23	416	20.0	499	21	AAV94875	Human potassium ch
24	416	20.0	499	22	AAE01026	Human TWIK-2 prote
25	416	20.0	511	22	ABG26753	Human TWIK-2 prote
26	397.5	18.1	155	20	AAV4132	Human TWIK-4 prote
27	386	18.6	313	20	AAV5116	Human TWIK-4 prote
28	386	18.6	313	20	AAV5116	Human TWIK-4 prote
29	386	18.6	313	21	AAV90355	Human TWIK-4 prote
30	386	18.6	313	21	AAV68737	Human TWIK-4 prote
31	386	18.6	313	21	AAV68738	Human TWIK-4 prote
32	386	18.6	313	22	AAE01028	Human TWIK-4 prote
33	379.5	18.3	336	18	AAW23397	Human TWIK-4 prote
34	379.5	18.3	336	21	AAV79673	Human TWIK-4 prote
35	377.5	18.2	383	22	ABG02731	Human TWIK-4 prote
36	361.5	17.4	361	22	ABG31805	Human TWIK-4 prote
37	353	17.0	1001	22	ABG58298	Human TWIK-4 prote
38	343	16.5	107	20	AAV28498	Human TWIK-4 prote
39	332.5	16.0	405	21	AAV95230	Human TWIK-4 prote
40	327.5	15.8	374	21	AAV18807	Human TWIK-4 prote
41	327.5	15.8	374	21	AAV18813	Human TWIK-4 prote
42	327.5	15.8	374	22	AAV63938	Human TWIK-4 prote
43	326.5	15.7	394	21	AAE10343	Human TWIK-4 prote
44	326.5	15.7	394	21	AAV79674	Human TWIK-4 prote
45	326.5	15.7	394	21	AAV87291	Human TWIK-4 prote

ALIGNMENTS

RESULT 1
AAV30647 standard; Protein: 398 AA.

AC AAV30647;
DT 18-NOV-1999 (first entry)

DE A mechanically sensitive potassium channel protein TRAK.

XX Mechanically sensitive potassium channel protein; TRAK;

KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;

KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;

KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;

KW muscular disease.

OS Mus sp.

PN WO9945108-A2.

PD 10-SEP-1999.

PF 23-FEB-1999; 99WO-FR00404.

PR 05-MAR-1998; 98FR-0002725.

PA (CNRS) CNRS CENT NAT RECH SCI.

PT Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;

DR WPI: 1999-551038/46.

XX N-PSDB: AA210606.

PT New mechanically sensitive potassium channel, used to screen for

PT specific modulators, potential therapeutic agents for heart and nervous
 XX system disorders
 PS Claim 2; Fig 1; 40pp; French.

XX The present sequence represents a mechanically sensitive potassium
 CC channel protein designated TPAK. The protein is activated by
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by
 CC riluzole. The protein is used to screen for specific modulators which
 CC are useful for treating or preventing diseases of the heart and nervous
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
 CC (arrhythmia), neurodegeneration (particularly where associated with
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular
 CC disease. The protein itself may be used to treat these diseases.
 CC Antibodies specific for the protein are used to detect it in tissues,
 CC also as therapeutic inhibitors or activators.
 XX Sequence 398 AA;

Query Match 100.0%; Score 2079; DB 20; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4e-169;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSTLLALALVLYVSGALVFOALPOHPOAKKMDHGRDQFLRDHPCVSQKSLSD 60
 Db 1 msttllalalvlyvsgalvfoalpoakkmhgrdqflrdhpcvsqksled 60
 QY 61 FIKLVEALGGANPETSWTSSNNSAMNLSAFAFFSGTITTTIGYGNVLTHTDAGRLF 120
 Db 61 fklvealgganpetswtssnnsamnlgsaffsgtitttlygnvlthtdagrlf 120
 QY 121 CIFVYALVGPILFQMLAGVGDRLGSSLRGIGHTEAFLKWHVPPGLVSLASVLFLLIG 180
 Db 121 cifvylvgpilfqlagvgrlgsrlrghieaflkwhvppglvslasvllfllig 180
 QY 181 CLFLVLTPTFVSFYSMESKLEATFYIVTLTVGFGDYVPGDGTGONSAPATOPVWMTI 240
 Db 181 clflvltptfvsfysmeskleaifyivtlvtvgfgdyvpgdgtgonsapatoptvwm 240
 QY 241 LFGATYFASVLTITGNMLRAVSRRTRAEMGGLTAQAASWTGVTARVYQRTGSPAPPEK 300
 Db 241 lfgatylfvtitgnmlravsrtrraemggltagaaswtgvtarvyrtrgspappek 300
 QY 301 EQLLPSSLPAPVAVPEPAGRGSPAPAKVETPSPPTASALDYPSENIAFIDESSPTOS 360
 Db 301 eqllpsslpavavepagspapekvetpsptasaldypsenlafidessdts 360
 QY 361 ERGCLPRAAPRGRRPNPSKPSRPRGRLRDKAAPV 398
 Db 361 ergclpraprrtrppskpsrprgrlrdkavpv 398

RESULT 2
 AAY94425
 ID AAY94425 standard; Protein: 393 AA.

AC AAY94425;
 XX 04-AUG-2000 (first entry)
 DE Human h-TPAK polypeptide #1.
 XX Human; h-TPAK; potassium channel polypeptide;
 KW 2p domain potassium channel; neurodegenerative disease; stroke;
 XX psychiatric disorder; neurological disorder; Gene therapy.
 OS Homo sapiens.
 XX
 PN W0200026253-A1.
 XX
 PD 11-MAY-2000.
 XX

PF 03-NOV-1999; 99WO-GB03634.

XX 03-NOV-1998; 98GB-0024048.

PR 07-OCT-1999; 99GB-0023668.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Chapman CG, Duckworth DM;

DR WPI: 2000-365583/31.

DR N-PSDB: AAA27105.

PT Novel isolated h-TPAK polypeptides belonging to the potassium channel

PT family of polypeptides, useful for the diagnosis and treatment of

PS h-TPAK related disorders, e.g. depression and schizophrenia

PS Claim 3; Page 21; 35pp; English.

XX Functional genomics was used to identify h-TPAK polypeptides and
 CC h-TPAK polynucleotides from human tissue samples. h-TPAK
 CC polypeptides have homology to the 2p domain potassium channel family of
 CC polypeptides. The h-TPAK polypeptides and polynucleotides may
 CC be used in diagnostic assays for conditions related to h-TPAK
 CC imbalance and for identifying agonists and antagonists of h-TPAK
 CC polypeptides. The h-TPAK polypeptides and polynucleotides may also
 CC be useful for treatment and prevention (e.g. as vaccines) of certain
 CC diseases, such as pain, psychiatric disorders including depression and
 CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke
 CC and head trauma and neurological disorders including migraine and
 CC epilepsy. The present sequence is human h-TPAK protein #1.
 XX Sequence 393 AA;

Query Match 81.4%; Score 1692.5; DB 21; Length 393;
 Best Local Similarity 82.4%; Pred. No. 3.8e-136;
 Matches 328; Conservative 24; Mismatches 41; Indels 5; Gaps 2;

QY 1 MRSSTLLALALVLYVSGALVFOALPOHPOAKKMDHGRDQFLRDHPCVSQKSLSD 60
 Db 1 msttllalalvlyvsgalvfoalpoakkmhgrdqflrdhpcvsqksled 60
 QY 61 FIKLVEALGGANPETSWTSSNNSAMNLSAFAFFSGTITTTIGYGNVLTHTDAGRLF 120
 Db 61 fklvealgganpetswtssnnsamnlgsaffsgtitttlygnvlthtdagrlf 120
 QY 121 CIFVYALVGPILFQMLAGVGDRLGSSLRGIGHTEAFLKWHVPPGLVSLASVLFLLIG 180
 Db 121 cifvylvgpilfqlagvgrlgsrlrghieaflkwhvppglvslasvllfllig 180
 QY 181 CLFLVLTPTFVSFYSMESKLEATFYIVTLTVGFGDYVPGDGTGONSAPATOPVWMTI 240
 Db 181 clflvltptfvsfysmeskleaifyivtlvtvgfgdyvpgdgtgonsapatoptvwm 240
 QY 241 LFGATYFASVLTITGNMLRAVSRRTRAEMGGLTAQAASWTGVTARVYQRTGSPAPPEK 300
 Db 241 lfgatylfvtitgnmlravsrtrraemggltagaaswtgvtarvyrtrgspappek 300
 QY 301 EQLLPSSLPAPVAVPEPAGRGSPAPAKVETPSPPTASALDYPSENIAFIDESSPTOS 360
 Db 301 eqllpsslpavavepagspapekvetpsptasaldypsenlafidessdts 360
 QY 361 ERGCLPRAAPRGRRPNPSKPSRPRGRLRDKAAPV 398
 Db 361 ergclpraprrtrppskpsrprgrlrdkavpv 398

RESULT 3
 AAY94426
 ID AAY94426 standard; Protein: 393 AA.
 AC AAY94426;
 XX

DT	04-AUG-2000 (first entry)	
XX	Human h-TRAAK polypeptide #2.	
DE		
XX	Human; h-TRAAK; potassium channel polypeptide;	
KW	2p domain potassium channel; neurodegenerative disease; stroke;	
KM	psychiatric disorder; neurological disorder; Gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200026253-A1.	
XX		
PD	11-MAY-2000.	
XX		
PF	03-NOV-1999; 99WO-GB03634.	
XX		
PR	03-NOV-1998; 98GB-0024048.	
PR	07-OCT-1999; 99GB-0023668.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM PLC.	
XX		
PI	Chapman CG, Duckworth DM;	
DR	WPI: 2000-365583/31.	
DR	N-PSDB; AAA27106.	
XX		
PT	Novel isolated h-TRAAK polypeptides belonging to the potassium channel	
PT	family of polypeptides, useful for the diagnosis and treatment of	
PT	h-TRAAK related disorders,e.g. depression and schizophrenia -	
PS	Claim 12; Pages 21 and 22; 35pp; English.	
XX		
CC	Functional genomics was used to identify h-TRAAK polypeptides and	
CC	h-TRAAK polynucleotides from human tissue samples. h-TRAAK	
CC	polypeptides have homology to the 2p domain potassium channel family of	
CC	polypeptides. The h-TRAAK polypeptides and polynucleotides may	
CC	be used in diagnostic assays for conditions related to h-TRAAK	
CC	imbalance and for identifying agonists and antagonists of h-TRAAK	
CC	polypeptides. The h-TRAAK polypeptides and polynucleotides may also	
CC	be useful for treatment and prevention (e.g. as vaccines) of certain	
CC	diseases, such as pain, psychiatric disorders including depression and	
CC	schizophrenia, neurodegenerative disease including Alzheimer's, stroke	
CC	and head trauma and neurological disorders including migraine and	
CC	epilepsy. The present sequence is human h-TRAAK protein #2.	
XX		
SQ	Sequence 393 AA:	
Query Match	81.4%; Score 1692.5; DB 21; Length 393;	
Best Local Similarity	82.4%; Pred. No. 3.8e-136; Indels 5; Gaps	
Matches 328;	Conservative 24; Mismatches 41;	
OY	1 MNSTLTALLAIVLYIVYSGALVFOALBOPHEQOAKMDHGRDQFLRHPCVSOKSLD 60	
DB	1 mrsstllaiaivlyivysgalvfralaeqphneqgqrgelgvrekflrahpcvdeqdlg 60	
OY	61 FIKLVEALVGGAGNETSWTNSNSNHSANWIGSAFFESGTTTTTIGYNIYLHMDAGRL 120	
DB	61 llikevadalggagdpetnstsnsnsh-sawdlgsaiffigtlltlygynvalrtcdagrl 119	
OY	121 CIFVALVGLPFCMLLAGCGDRUGSLRNGIGHIEAFIKWHPVPGALVRSASVLELLIG 180	
DB	120 cifaivaivpflfiglilaavgdrlgssllringihieaiflkwnvpelrvtsamlfllig 179	
OY	181 CLLEVLTPTFVFSYMSWSKLEIAIEVIVITLTGFGDVPEDDGTGQNSPAPOLVWPMI 240	
DB	180 clilvlpptfvcymedwskleiaievivltlttvgfgdyvaagadpqpdsapayqplvwmi 239	
OY	241 LFGIALVPSAVLTITGNMLRAVSRRTAEKMGCLTAAQAASTGVTAVTQRTQSPAPPEK 300	
DB	240 llglaylasvltitgnmlravsvrrtaekmgllaqaasvtgvtatvtrqraqpaapppek 299	
OY	301 EGPLPSSLPAAPVAVPEAGHPGSPAPAEKVEVTPSPPTASALDYPSENLAFIDESSDTS 360	

Db 300 exp1-----|ppppcagqlgrrpspspekaqppspptalsaldysenalfideasttgs 355

Qy 361 ERGCAIPRAPRGRRRPNFSKSKSRPRGCGRLDKRANPV 398

Db 356 ergcplpraprgrrrrpprpkvrrpsrgpridkqygv 393

RESULT 4

AA667777 standard; protein; 393 AA.

AC AAG67777

DT 10-DEC-2001 (first entry)

XX DE Human mechanically sensitive potassium channel hTRAK polypeptide.

XX Human; mechanically sensitive potassium channel; riluzole; TWICK;
KW L-glutamic acid; arachidonic acid; hTRAAK; chromosome 11q13;

polyunsaturated fatty acids; anoxia;
KW neuromuscular excitation; muscle
excitation; cardiac rhythm; ischemia;

KW hormone secretion; cardiac disease; vascular disease; muscle disease; endocrine disorder; endocrinopathies

retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration

OS Homo sapiens.

PN WO200168670-A2

20-SEP-2001.

14-MAR-2001; 2001WO-FR00758

AA
PR 14-MAR-2000; 2000FR-0003264

XX
PA
(CNRS) CNRS CENT NAT RECH SCI.

xx Lazdunski M, Lesage F, Maingret F;
PI

XX
DR
WPI: 2001-590037/66.

DR WFL, 2001-09-08, 1
N-PSDB; AAH78636, AAH78646.
DR

AA New mechanically sensitive potassium channel, useful for treating
PT is activated by

polyunsaturated fatty acids

XX
PS
Claim 1; page 34-35; 37pp; French.

XX
CC The present sequence represents a human mechanically sensitive potassium

The polypeptide is designated CC channel which is secreted by riluzole. The polypeptide is designated CC arachidonic acid (AA) and by riluzole. The hTRAAK

human TWIK related kinase 1 (hTRAK) is involved in regulation of the insulin-like growth factor-1 (IGF-1) gene is located on chromosome 11q13.

of neuronal and muscle contractile proteins. The *hTRAK* gene, designated to screen for modulators of neuronal and muscle contractile proteins, was found to be useful for prevention of neuronal and muscle contractile proteins.

of HIRAAN activity. Such measurement of HIRAAN activity, in humans and animals, of treatment, in humans and animals, of cardiac and/or vascular disease, or treatment, in humans and animals, of endocrinological and/or endocrine disease, or treatment, in humans and animals, of

diseases associated with anomalous hormone secretion or muscle diseases;

CC and retinal diseases: typical examples

XX	Sequence	393 AA:
EQ		

Query Match	81.4%	Pred. No. 3.8e-136;
Post Local Similarity	82.4%	

Matches	328;	Conservative	27,	Labour	251
					1970-1974
					1975-1979
					1980-1984
					1985-1989
					1990-1994
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					2020-2024
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					2030-2034
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					2045-2049
					2050-2054
					2055-2059
					2060-2064
					2065-2069
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					2075-2079
					2080-2084
					2085-2089
					2090-2094
					2095-2099
					2100-2104
					2105-2109
					2110-2114
					2115-2119
					2120-2124
					2125-2129
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					2160-2164
					2165-2169
					2170-2174
					2175-2179
					2180-2184
					2185-2189
					2190-2194
					2195-2199
					2200-2204
					2205-2209
					2210-2214
					2215-2219
					2220-2224
					2225-2229
					2230-2234
					2235-2239
					2240-2244
					2245-2249
					2250-2254
					2255-2259
					2260-2264
					2265-2269
					2270-2274
					2275-2279
					2280-2284
					2285-2289
					2290-2294
					2295-2299
					2300-2304
					2305-2309
					2310-2314
					2315-2319
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					2360-2364
					2365-2369
					2370-2374
					2375-2379
					2380-2384
					2385-2389
					2390-2394
					2395-2399
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					2405-2409
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					2455-2459
					2460-2464
					2465-2469
					2470-2474
					2475-2479
					2480-2484
					2485-2489
					2490-2494
					2495-2499
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QY 1 MRSTLLALLVLLVSGHVLQRLDQ... 1:11 1111 : 1

Db 1 mrs t l i a l i v y s g a r n a c q p a c f f f f f f f

RESULT	5
AAU04571	
ID	AAU04571 standard; Protein; 1314 AA.
XX	

AC	AAU04571;
XX	
DT	17-DEC-2001 (first entry)
XX	

Human G-protein coupled receptor like protein, GPCR #8.

Human; G-protein coupled receptor like protein; GPCR; immunogen;
ophthalmic disease; neurological disease; Alzheimer's disease;
Parkinson's disease; immunological disorder; HIV; candidiasis;
human immunodeficiency virus; autoimmune disorder; multiple sclerosis
systemic lupus erythematosus; rheumatoid arthritis; platelet disorder
thrombocytopenia; aplastic anaemia; inflammatory disorder;
septic shock; systemic inflammatory response syndrome; SIRS;
hormonal dysfunction; cancer; atherosclerosis; wound;
tissue regeneration; haemophilia; leukaemia; reperfusion injury;
psoriasis; diabetes; h-TRAK polypeptide #1.

R		Homo sapiens.
X	CS	
X		
FN	W020153454-A2.	
D		
D	26-JUL-2001.	
F		
P	22-DEC-2000; 2000MO-US34983	
X		
X	21-JAN-2000; 2000US-OA88725	
X	25-APR-2000; 2000US-0552317	
R	20-JUN-2000; 2000US-0598042	
R	13-JUL-2000; 2000US-0620312	
R	31-AUG-2000; 2000US-0653450	
R	04-DEC-2000; 2000US-0729739.	

(HYSE-) HYSEQ INC.

Yamazaki V, Tang YT, Liu C, Zhou P, Wang D, Zhang J, Ren F, Asundi V, Drmanac RT;

WPI; 2001-442255/47.
N-PSDB; AAS08652.

New G-protein-coupled receptor-like polypeptides and polynucleotides, useful for treating diseases of ophthalmic, neurological, immunological, and nephritic systems and hormonal dysfunction, cancer, atherosclerosis, and diabetes -

XX The sequence represents a human G-protein coupled receptor (GPCR)-like
PS protein, found to be homologous to human h-TRPAK polypeptide #1.
XX The GPCR-like polypeptides and polynucleotides are useful for
CC the treatment of diseases of ophthalmic, neurologic (e.g. Alzheimer's
CC disease and Parkinson's disease, immunological (e.g. HIV infection and
CC candidiasis), autoimmune disorders (e.g. multiple sclerosis, systemic
CC lupus erythematosus and rheumatoid arthritis), platelet disorders (e.g.
CC thrombocytopaenia and aplastic anaemia), inflammatory disorders (e.g.
CC septic shock and systemic inflammatory response syndrome, SIRS) and
CC nephritic systems. They may also be used to treat hormonal dysfunction,
CC cancer, atherosclerosis, wounds, tissue regeneration, haemophilia,
CC leukemias, reperfusion injury, psoriasis and diabetes. Numerous examples
CC of each type of disorder are given in the specification. Anti-GPCR-like
CC protein antibodies are useful for detecting or quantitating the
CC polypeptide in tissue. The polypeptides can also be used as molecular
CC weight markers and as a food supplement.
XX
XX Sequence 1314 AA;
50

Query Match	81.2%	Score 1688.5;	DB 22;	Length 1314;
Best Local Similarity	82.4%;	Pred No. 3.7e-135;		
Matches 327; Conservative	24;	Mismatches 41;	Indels 5;	Gaps 2

QY I MSTSTLLALLVLTLYIVSGALVFQALEDPEHEDQAOKKMDRDFLELDHPHCVSOKSLSD 60
|||||
540 msttllallalvilyvsqalvtfraleqphqqagrelgevrektflrahpcvsdgelg 59g

61 FIKLVEALGGANPETSWTNNSSHHSSAMNLGCAFFFSGITITTTIGYGNIVLHTDAGRLF 120

121 CIPFALVGIPLEFGLLAGVDRGLSSLRGICIEATETKEHVDDCIYRQCSVMPLLEK 658

Db 659 cffyaIvqiprlfgllagygdrlgsslrhngighteaiflkwhvpe|vrv|sam|fll|c 718

181 CLFLVLTPTFEFSYMESWSKLEAIYFVILVLTITVGFGDYVPDGTGQNSPAYQPLVMEI 240

719 cllvltpitvfcymedwskleailyfvlvltvtvgfdyvagadprgdspayqplvwfwl 778

779 LFGAVFASVLITIGNWLEAVSRRTRAENGGLTQAASWTGVTARATORTGPSAPPEK 300

301 EQPLPSSLAPPAVEAGRPGSPABAEKVETPSDEPTASAIIDYPSNMI AETDEGCTTCTG 300

[illegible]

361 ERGALPRAPGRRRPNPSKKPSRPRGPGRLDKAVP 397
||||| :|||

895 ergcplpraprrrrnpnrpkvprpgrprdkgvp 931

ESULT 6
BB12229

D ABB12229 standard; peptide: 421 AA.
x ABB12229.
x

11-JAN-2002 (first entry)

Human K channel TRAAK homologue, SEQ ID NO:2599.

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; transcription factors

inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoiesis; tissue growth; immunomodulator; activin; cell regulation; cytokine

myeloid cell disorder; lymphoid cell disorder; asplasia; arthritis; chronic inflammatory condition; proliferative retinopathy; attherosclerosis

arteriosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antihistaminic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteoprotic; vasotropic; cardiac; virucide; antibacterial;
 KW antifungal; vulnereary; antitumor.

OS Homo sapiens.

PN WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-0503800.

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX (HXSE-) HXSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-457740/49.

DR N-PSDB; ABA09473.

PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -

PS Claim 20; Page 318; 1963pp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders to
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

XX Sequence 421 AA;

Query Match 43.0%; Score 895; DB 22; Length 421;

Best Local Similarity 70.3%; Pred. No. 4.5e-68;
 Matches 182; Conservative 18; Mismatches 19; Indels 40; Gaps 2;

OY 1 MNSTLLALLALVLYVSGALVLPQALPEPHQOAKQKMDHRDQFLRBDHPVSGSKLED 60
 DB 163 mstllallallvlyvsgalvlpqalpephqoqreqlvexrefllanpcvsdqelgl 222
 OY 61 FIKLVEALGGGANPEPTSMNSNHSANMLGSAFFSGTITTTI----- 105
 DB 223 lkevaldaggadpetnsmsh-sawdlgsaffsgtltttlggggdwhvggkelp 281
 OY 106 -----GYGNIVLHTDAGRLFCIFYALVGLPFLGMLLAGVD 141
 DB 282 hggcreteggsvaprlpsaplcpgygnvalrtdaqrlfcifyalvgplfigllla9ygd 341
 OY 142 RLCSSLRKRGIGHLEALFLKWHVPPGLVRSLSAVLFLICGLLEFVLPFVFSYMSWSKL 201
 DB 342 rlgsrlrhghleaalflkwhvpplvrlsamllilicglilfvltptvfcymedwskl 401
 OY 202 EATYFVIVTLTVGFQDYY 220
 DB 402 ealYfVIVtlTVgfQdy 420

RESULT 7

ID AAY34133 standard; Protein; 411 AA.

AC AAY34133;

DT 30-NOV-1999 (first entry)

XX Human potassium channel K-Hnov59.

KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KW cardiovascular disorder; CNS disorder; renal disorder.

OS Homo sapiens.

PN WO9943696-A1.

PD 02-SEP-1999.

PF 22-FEB-1999; 99WO-US03826.

PR 19-JAN-1999; 99US-0116448.

PR 25-FEB-1998; 98US-0076687.

PR 07-AUG-1998; 98US-0095836.

PA (AAYS-) AAYS PHARM INC.

PI Curran ME, Hu P, Miller AP, Rutler M, Wang J;

DR WPI; 1999-527591/44.

DR N-PSDB; AAZ11915.

PT New nucleic acids encoding mammalian K-Hnov potassium channel
 PT proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome

PS Claim 3; Page 104-105; 112pp; English.

XX This sequence represents the human K-Hnov59 potassium channel.
 CC K-Hnov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate the channel activity. K-Hnov59
 CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene
 CC is located on chromosome 19, determined via PCR chromosomal
 CC localisation using primers AAZ11939 and AAZ11940. K-Hnov cDNAs
 CC were isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple
 CC independent clones. Potassium channels have critical roles in various

cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymia; cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical components of virtually all cells, it is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) disorders. Nucleotides encoding K+Hv proteins may be used for identifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hv protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K+Hv protein in fermentation cultures. Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.

Sequence 411 AA;

Query Match	37.3%	Score	776.5	DB	20	Length	411
Best Local Similarity	49.8%	Pred. No.	5.7e-58				
Matches	142	Conservative	83	Indels	3	Gaps	1

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QY 1 MRSFTLLALLLVLLVYVSGALVTCQALVEOPHEQDAOKMKHGRQRLRDPVCSQKLED 60
D 42 mkwktvctiflvvlyllilgvtvkaleqphelsqrtillykqtkitlsgnsavnsleld 1010
QY 61 FIKLLVEALGGGAPMETSMTNSSNHHSSAMNLGSAFPFSGTITTTIGYGNLTHTDAGRLF 1207
D 102 lllgqivaahmagllp--lqntsqibshwdlsgsfagvtvltlllggnlsptegskif 158
QY 121 CIEFALVGIPFLGMLLAGVGDRLGSSLRRGHTEALFELMNHVPRGLVRSLSAVLFLITG 1807
D 159 cilyalligplfglllsgvqdqlygultfgkqakaveditflkwnvsqtkiristctifllfg 218
QY 181 CLLEFVLTPTFEVSYSMSKLEALYEVTVLTVTGFEEDYPPGCGTGQNSPAYQLEFWFI 240
D 219 cvlfvalpalafllkhllegwsaldaifyfvltitctlltfgdygaagsdleyldfypvwfwl 278
QY 241 LFGFALVPAVLTITGNMLRAVSRTRAEMLGCLTAQAASTWGTGYTA 285
D 279 lvgldayfaavlysmgdwlvlvlskkkeeygefahaahevaanta 323

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RESULT	8
AAV28496	
ID	AAV28496 standard; Protein; 411 AA
YV	

AC AAY28496;

DT 12-OCT-1999 (first entry)
 YY

h-TREK1 polypeptide.

h-TREK1; two pore potassium channel; inflammatory disease; chromosome 1q32.

Homo sapiens.

PN W09937762-A1.

PD 29-JUL-19

02-DEC-1998; 98WO-EP07805.

PR 09-OCT-1998; 98GB-0022135.
PR 27-JAN-1998; 98ED 0300570

27-JAN-1998; 98EP-0300570.

(SMIK) SMITHKLINE BEECHAM PLC.

Chapman CG, Meadows HJ;

DR WPI; 1999-469126/39

DR N-PSDB; AAZ00039

XX New two pore potassium channel used for, e.g. treatment of cancer
 PI pulmonary, cardiovascular and inflammatory diseases
 XX
 PS Claim 3; Page 24; 44pp: English.

Claim 3; Page 24; 44pp; English

CC This sentence is the h-TREK1 polypeptide, encoded by the h-TREK1
CC polynucleotide AA200033. h-TREK1 is a two pore potassium channel, and
CC the gene maps to human chromosome 1q32, between the markers DIS237 and
CC M15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC disease or susceptibility to a disease related to expression or activity
CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the
CC treatment of diseases including cancer, pulmonary, cardiovascular, and
CC inflammatory diseases, pain, psychiatric disorders including depression
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC stroke, and head trauma and neurological disorders including migraine.

Sequence 411 AA;

Query Match	37.38;	Score 776.5;	DB 20;	Length 411;
Best Local Similarity	49.88;	Pred. No. 5.7e-58;		
Matches 142;	Conservative 57;	Mismatches 83;	Indels 3;	Gaps 1;

[illegible]

RESULT	9
AAE10341	
ID	AAE10341 standard; Protein; 411 AA

AAE10341;

DT	10-DEC-2001	(first entry)
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Human TREK-1 potassium channel protein.

Human; potassium channel protein; TREK-1; anaesthetic; analgesia; amnesia.

05 Homo sapiens.

PN WO200047738-A2

PD 17-AUG-2000.

11-FEB-2000; 2000WO-IB002226.

PR	12-FEB-1999;	99US-0119727.
PR	11-FEB-2000;	2000US-0503060

11-FEB-2000; 2000US-0503089.

(CNRS) CNRS CENT NAT RECH SCI.

Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;

; GENERAL INFORMATION.

APPLICANT: Helen Meadows
 APPLICANT: Conrad Chapman
 TITLE OF INVENTION: No. 6242217e1 Compounds
 FILE REFERENCE: GP30031
 CURRENT APPLICATION NUMBER: US/09/236,080
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 6
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-236-080-6

Query Match
 Best Local Similarity 37.1%; Score 770.5; DB 4; Length 411;
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;

OY 1 MRSTLLALLAVLYLVSGALVFOALPOHEQOAKMDHGRDQFLRHPVCSOKSLD 60
 DB 42 MKMKVSTIFLVVLYLIGAVFKALEPOEISORTTIVIOKOTFLAHCYNSTELDE 101
 OY 61 FIKLVEALGGANPETSWTSSNHSAMNLSAFFFSGTITITIGYGNVLTDAGRLE 120
 DB 102 LIQOIVAAINAGIIP---LGSSNOVSHMDLSSFFAGVITITIGGNISPRTEGKTF 158
 OY 121 CIFVALGIPLEGMLAGVGRIGSLRGIGHEAIFLKMVPPGLVRSLSAVFLILG 180
 DB 159 CIYALGIPLEGFLAGVGDQGTIFGKIAKVEDTFIKMVSQTKIRIITIFILFG 218
 OY 181 CLFVLPTFFVFSWESKLEAIFYVLTGVGFDVPGDGTGNSPAVOPLYMWI 240
 DB 219 CVLFAVLPVTFKHIEGMSALDAIFYVLTITIGFDYVAGSDIEYIDFKPVVWMI 278
 OY 241 LFGIAYFASVLTITGNMLRAVSRRTRAEMGGLTQAASMTGVTA 285
 DB 279 LVGLAYFAAVLSMIGDMLRVISKTKKEVEGFRHAHAEMTANVTA 323

RESULT 3
 US-09-144-914-8
 Sequence 8, Application US/09144914
 Patent No. 6309855
 GENERAL INFORMATION:
 APPLICANT: Duprat, Fabrice
 APPLICANT: Lesage, Florian
 APPLICANT: Pink, Michel
 APPLICANT: Lazdunski, Michel
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
 FILE REFERENCE: 989, 6705CIP
 CURRENT APPLICATION NUMBER: US/09/144, 914
 EARLIER FILING DATE: 1998-09-01
 EARLIER APPLICATION NUMBER: 08/749, 816
 EARLIER FILING DATE: 1996-11-15
 EARLIER APPLICATION NUMBER: 60/095, 234
 EARLIER FILING DATE: 1998-08-04
 EARLIER APPLICATION NUMBER: FR 96/01565
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 8
 LENGTH: 370
 TYPE: PRT
 ORGANISM: Murine
 FEATURE:
 OTHER INFORMATION: TREK-1
 US-09-144-914-8

Query Match
 Best Local Similarity 36.6%; Score 761.5; DB 4; Length 370;
 Pred. No. 3.8e-56;

Matches 141; Conservative 56; Mismatches 85; Indels 3; Gaps 1;
 OY 1 MRSTLLALLAVLYLVSGALVFOALPOHEQOAKMDHGRDQFLRHPVCSOKSLD 60
 DB 42 MKMKVSTIFLVVLYLIGAVFKALEPOEISORTTIVIOKOTFLAHCYNSTELDE 101
 OY 61 FIKLVEALGGANPETSWTSSNHSAMNLSAFFFSGTITITIGYGNVLTDAGRLE 120
 DB 102 LIQOIVAAINAGIIP---LGSSNOVSHMDLSSFFAGVITITIGGNISPRTEGKTF 158
 OY 121 CIFVALGIPLEGMLAGVGRIGSLRGIGHEAIFLKMVPPGLVRSLSAVFLILG 180
 DB 159 CIYALGIPLEGFLAGVGDQGTIFGKIAKVEDTFIKMVSQTKIRIITIFILFG 218
 OY 181 CLFVLPTFFVFSWESKLEAIFYVLTGVGFDVPGDGTGNSPAVOPLYMWI 240
 DB 219 CVLFAVLPVTFKHIEGMSALDAIFYVLTITIGFDYVAGSDIEYIDFKPVVWMI 278
 OY 241 LFGIAYFASVLTITGNMLRAVSRRTRAEMGGLTQAASMTGVTA 285
 DB 279 LVGLAYFAAVLSMIGDMLRVISKTKKEVEGFRHAHAEMTANVTA 323

RESULT 4
 US-08-749-816-2
 Sequence 2, Application US/08749816
 Patent No. 6013470
 GENERAL INFORMATION:
 APPLICANT: Lesage, Florian
 APPLICANT: Guilleme, Eric
 APPLICANT: Pink, Michel
 APPLICANT: Duprat, Fabrice
 APPLICANT: Lazdunski, Michel
 APPLICANT: Romey, Georges
 APPLICANT: Barhanin, Jacques
 TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
 TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEISER & ASSOCIATES
 STREET: 230 South Fifteenth Street, suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/749, 816
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.
 REGISTRATION NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 989, 6351P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8394
 TELEFAX: 215-875-8394
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-749-816-2

Query Match
 Best Local Similarity 18.3%; Score 379.5; DB 3; Length 336;
 Pred. No. 3.4e-24;

Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

OY 2 RSTLLALLAL-VLLYVSGALVQALQEPHEDQAKKMDHGRDQFLRHPQVSKSLD 60
 Db 18 RSAMCFGLVGLYLLVFGAVFSSVELPEYEDLLRQELKRLRLEHECLSEQDLQ 77

OY 61 FIKLLVEMAGG---ANPETSMTNSNHNSSANNLGSAPFSGTITTTGYNIVLHTDA 116
 Db 78 FLGRVLESNNGSVLSNAGNNM-----WDFTSALFFASTVLTSTGCHTVP LSDG 129

OY 117 GRLECFIYALVIGPLFGMLAGVDRGSSL-RRGIGHIAIFLKMVPPGLVRSLSAVL 175
 Db 130 GKAFCIIVSVIGIPFTLLFTAVVQRTVHTRRVLYFH---IRMGFSQVVAIVHAVL 186

OY 176 --FLILGCLLVLPFTFVSFME-SWSKLEAIVFVITLTTFVGFGDVPDGTGON-SPA 231
 Db 187 LGFVTVSCFFFL--PAAVSVLEDDWNFLSFYCFISLSTIGLDIVPDEGINQKREL 244

OY 232 YQPLVFWILFGLAFASVLT 253
 Db 245 YKIGITCYLLGLLMLVLET 266

RESULT 5
 US-09-144-914-2
 ; Sequence 2, Application US/09144914
 ; Patent No. 6309855
 ; GENERAL INFORMATION:
 ; APPLICANT: Duprat, Fabrice
 ; APPLICANT: Lesage, Florian
 ; APPLICANT: Fluk, Michel
 ; APPLICANT: Lazdunski, Michel
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
 ; FILE REFERENCE: 989,6705CIP
 ; CURRENT APPLICATION NUMBER: US/09/144,914
 ; CURRENT FILING DATE: 1998-09-01
 ; EARLIER APPLICATION NUMBER: 08/749,816
 ; EARLIER FILING DATE: 1996-11-15
 ; EARLIER APPLICATION NUMBER: 60/095,234
 ; EARLIER FILING DATE: 1998-08-04
 ; EARLIER APPLICATION NUMBER: FR 96/01565
 ; EARLIER FILING DATE: 1996-02-08
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 336
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: TWIK-1
 US-09-144-914-2

Query Match 18.3%; Score 379.5; DB 4; Length 336;
 Best Local Similarity 34.4%; Pred. No. 3.4e-24;
 Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

OY 2 RSTLLALLAL-VLLYVSGALVQALQEPHEDQAKKMDHGRDQFLRHPQVSKSLD 60
 Db 18 RSAMCFGLVGLYLLVFGAVFSSVELPEYEDLLRQELKRLRLEHECLSEQDLQ 77

OY 61 FIKLLVEMAGG---ANPETSMTNSNHNSSANNLGSAPFSGTITTTGYNIVLHTDA 116
 Db 78 FLGRVLESNNGSVLSNAGNNM-----WDFTSALFFASTVLTSTGCHTVP LSDG 129

OY 117 GRLECFIYALVIGPLFGMLAGVDRGSSL-RRGIGHIAIFLKMVPPGLVRSLSAVL 175
 Db 130 GKAFCIIVSVIGIPFTLLFTAVVQRTVHTRRVLYFH---IRMGFSQVVAIVHAVL 186

OY 176 --FLILGCLLVLPFTFVSFME-SWSKLEAIVFVITLTTFVGFGDVPDGTGON-SPA 231
 Db 187 LGFVTVSCFFFL--PAAVSVLEDDWNFLSFYCFISLSTIGLDIVPDEGINQKREL 244

OY 232 YQPLVFWILFGLAFASVLT 253
 Db 245 YKIGITCYLLGLLMLVLET 266

RESULT 6
 US-09-236-080-4
 ; Sequence 4, Application US/09236080
 ; Patent No. 6242217
 ; GENERAL INFORMATION:
 ; APPLICANT: Helen Meadows
 ; APPLICANT: Conrad Chapman
 ; TITLE OF INVENTION: No. 6242217el Compounds
 ; FILE REFERENCE: GP30031
 ; CURRENT APPLICATION NUMBER: US/09/236,080
 ; CURRENT FILING DATE: 1999-01-25
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-236-080-4

Query Match 16.5%; Score 343; DB 4; Length 107;
 Best Local Similarity 58.1%; Pred. No. 8.7e-22;
 Matches 61; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

OY 81 NSSNHNSSANNLGSAPFSGTITTTGYNIVLHTDAGLRFIFALVIGPLFGMLAGV 140
 Db 1 NSSNQSWMDLGSSFFFACTVITTFGNISPRTEGKIFCIITVALLGIPFGMLAGV 60

OY 141 DRGSSLRGIGHIAIFLKMVPPGLVRSLSAVLFLIGCLLV 185
 Db 61 DQGTIFGKIAKVEDTFIKMVSQTKIRIITITIFLFGCLV 105

RESULT 7
 US-09-144-914-5
 ; Sequence 5, Application US/09144914
 ; Patent No. 6309855
 ; GENERAL INFORMATION:
 ; APPLICANT: Duprat, Fabrice
 ; APPLICANT: Lesage, Florian
 ; APPLICANT: Fluk, Michel
 ; APPLICANT: Lazdunski, Michel
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
 ; FILE REFERENCE: 989,6705CIP
 ; CURRENT APPLICATION NUMBER: US/09/144,914
 ; CURRENT FILING DATE: 1998-09-01
 ; EARLIER APPLICATION NUMBER: 08/749,816
 ; EARLIER FILING DATE: 1996-11-15
 ; EARLIER APPLICATION NUMBER: 60/095,234
 ; EARLIER FILING DATE: 1998-08-04
 ; EARLIER APPLICATION NUMBER: FR 96/01565
 ; EARLIER FILING DATE: 1996-02-08
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Murine
 ; FEATURE:
 ; OTHER INFORMATION: TASK
 US-09-144-914-5

Query Match 16.0%; Score 332.5; DB 4; Length 405;
 Best Local Similarity 31.6%; Pred. No. 3.8e-20;
 Matches 85; Conservative 44; Mismatches 97; Indels 43; Gaps 7;

```

0Y 7 LALLALVLYVSGALFOALLPDRPHQQAOKKDHRRDOFLRDHPCVSOXSLEDFIKLLV 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 6 LALIVCFITYLTVAAVFDALBESPEPIERQREI-ROLELARYNLSEGGVEELERVYL 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 67 EALGGANPETSWTNSSNHHSSAMNLLGSAFFFSQITITTYGNYILHFDAGRCIFPAL 126
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 RLKPHKAGVO-----WRFGSEFYAIVTITTYGHAAPSTDGSKVCMETAL 112
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 127 VGIFLFMLLAGVDRGLSRL-----RGIG--HIEAIFLKMHPVGLYRSJAVLFL 177
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 113 LGIFLITIMQSLGERINTVRLILHRAKRGJGMRIAE-----YSMANVLLIG 160
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 178 LIGLLVLPVLPVTFEYSMESKLEAIVYVLTITVFGSDV--PCDGTGONSAPVQPL 235
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 FVSGISFLICGAAGAFSYEKEWTFEFOAYYCFITLTTIGSDVVALOKQOALQTPQY--- 217
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 236 VWEIILFGIAFASVLTITGNMLRAVSR 264
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 218 ---VAFSFIYILGLTVIGAFELNVLVR 242
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT      8
US-09-144-914-4
; Sequence 4, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Pink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TASK
US-09-144-914-4

```

[illegible]

```

QY 235 LVMENILFGLAYFASVLTITGNMIRAVSR 264
      : | | : | | | : | |
Db 221 ----VAFSFYVLTGLITVIGAFNLVYL 245

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1      RESULT      9
2      US-08-332-312-2
3      ; Sequence 2, Application US/08332312
4      ; Patent No. 5559026
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Price, Laura A.
8      ; APPLICANT: Pausch, Mark H.
9      ; TITLE OF INVENTION: Functional Expression of a Drosophila
10     ; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
11     ; NUMBER OF SEQUENCES: 4
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: American Cyanamid Company
14     ; STREET: One Cyanamid Plaza
15     ; CITY: Wayne
16     ; STATE: New Jersey
17     ; COUNTRY: US
18     ; ZIP: 07470-8426
19     ;
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOOS
24     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/08/332,312
27     ; FILING DATE:
28     ; CLASSIFICATION: 435
29     ; ATTORNEY/AGENT INFORMATION:
30     ; NAME: Harrington, James J.
31     ; REGISTRATION NUMBER: P-39,711
32     ; REFERENCE/DOCKET NUMBER: 32,421
33     ; TELECOMMUNICATION INFORMATION:
34     ; TELEPHONE: 201-831-3246
35     ; TELEFAX: 201-831-3305
36     ; INFORMATION FOR SEQ ID NO: 2:
37     ; SEQUENCE CHARACTERISTICS:
38     ; LENGTH: 618 amino acids
39     ; TYPE: amino acid
40     ; TOPOLOGY: linear
41     ;
42     ; MOLECULE TYPE: protein
43     ;
44     ; US-08-332-312-2

```

Query Match	14.5%	Score 301.5	DB 1	Length 618
Best Local Similarity	27.7%	Pred. No. 2,6e-17		
Matches	91	Conservative 51	Mismatches 11	Indels 75
				Gaps 10
QY	7	LALLALVLLVSGALVFGALRQPHROQAQRKMDHDDOFLDHPHCVSQKSLSEDFKILY	66	
DB	7	ILLIFYIIVLMFGAIIYHIE-----HGEKISRAEQKQAIANEY---LL	51	
QY	67	EALGG-----ANPETSTNNSNHSAAMLCSAFPFSGTIIITIGYNI	110	
DB	52	EELGDKNTTODEIIQRIISDYCDKRPVTLRPTDYDDPYTFTEFHAFFFAFVCSIVGYNI	111	
QY	111	VLAHDAGRLFCFEVALVGIPLFGMLLAGDGLSSLRIGIHIAFIKMW-----	161	
DB	112	SPTTAGRMIMAIYSVIGIPVNGILFAGIGEFYGT-----FAIIRRRKKRYKMSIDM	164	
QY	169	-HVPBGVYKSLSAVYFLILGCLLEVLPLPF-VESYMESMKLEALYFVIVLTVTGFGDY	219	
DB	165	HVPPQLGLITTTVIALIPGALFVLPCVGHILRELGLSISISYVTTTIGFDY	224	
QY	220	VPGDSTGQNSP-----AYOPLVWMIIFGLAYFASVLTITGNMLRAARSRKTRAEMLGT	273	
DB	225	VPTFGANQPKREGGFVYVQILFVIVWFLEFSIGLYLMIWMTFTTIGLOS-----KRLAYLE	278	
QY	274	AQAAS-----WTGTVTARVQTORTG	292	

RESULT 13
US-08-749-816-3
Sequence 3, Application US/08749816
Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemaire, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunski, Michel
APPLICANT: Romey, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996

```

RESULT 14
; US-09-144-914-6
; Sequence 6, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; EARLIER FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
; US-09-144-914-6

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Query Match 8.9%; Score 184.5; DB 4; Length 347;
Best Local Similarity 25.8%; Pred. No. 7.7e-08;
Matches 69; Conservative 41; Mismatches 74; Indels 83; Gaps 11;

QY 6 LLAALAVLVVSGALVFQALQEPHQOAKMDHGRDQFLRDHPVCVSOSELEDFIKL 65
DB LSAITLVLEFLI-GAGIFVLAETQNSSES-----LNNSNVS-KCLHNL----- 82
QY 40 LSAITLVLEFLI-GAGIFVLAETQNSSES-----LNNSNVS-KCLHNL----- 82
DB 66 VEALGGANPETS-----WTNSNHSANMLGSAFFSGTITITIGINIVLHTDAGRL 119
QY 83 --PIGGKITAEKSKIKLCKLTKSRID--GFGKAIFFSWTLVSTVGSLYPHSTLGRY 137
DB 120 FCIFYAVLGPPL-----FCMLAG-----VGDRLGSSLR-----GI 151
QY 138 LTFYSLMTVFIAFKEFETFLAHLVYVSNRTLAVKAYKLSQNPENAEPTPSNL 197
DB 152 GHIAFLKMHVPPGLVRSIAVLELLIGCLLFLVPTFFSVYSMSKLEAIVFVITL 211
QY 198 QHDYLIPLS-----SLLCSISLSSALFSSITENISYLSVYFGITM 241
DB 212 TTVGFGDYVPDGTGQNSPAYQPLWF 238
QY 242 FLIGIDIVPTN-----LWVF 257

RESULT 15

US-08-906-865-4

Sequence 4, Application US/08906865

Patent No. 6040168

GENERAL INFORMATION:

APPLICANT: Greengard, Paul

APPLICANT: Porton, Barbara

APPLICANT: Kao, Hung-Teh

TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,865

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 696 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: /desc = "Synapsin Ia"

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

Query Match 6.3%; Score 132; DB 3; Length 696;
Best Local Similarity 28.8%; Pred. No. 0.0048;
Matches 42; Conservative 16; Mismatches 42; Indels 46; Gaps 5;

QY 289 QRTGP---SAPPEKEQPL-----LPSLPPAPVAVP----- 318
DB 475 QROGPPLOQRPPPOGOHLSGLCPPAGSPLPQRLPSPTAPQOQASQAAPPPTQGGGROSR 534
QY 319 --AGRGPSPAPAEKVTETPSPPTASALDYPSENLAFTDESSDQSERGALPRA---PRG 372
DB 535 PVAGGPGCAPPAAPPAAPASPS-----QROAGPPQATRTQTSVSGPAPAPKASGAPPG 584
QY 373 RRRPNPSKKRSPRPGRLDKAVPV 398
DB 585 QOROGPPQKRPAGPPTROASQAGPV 610

Search completed: June 4, 2002, 11:00:34

Job time: 124 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2002, 10:58:45 ; Search time 20.89 Seconds
(without alignments)
1830.711 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 2079
Sequence: 1 MRSFTLLALLLVLLVIVG.....SKPSRPRGRLRDKAVPV 398

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	379.5	18.3	336	2	S65566 inward rectifier p
2	353	17.0	1001	2	T13807 potassium channel
3	323.5	15.6	330	2	TC7703 TASK-5 protein - h
4	322	15.5	329	2	T43509 probable potassium
5	314.5	15.1	336	2	T32347 outward rectifier
6	298.5	14.4	364	2	T43361 probable potassium
7	291.5	14.0	334	2	T19860 hypothetical prote
8	279	13.4	528	2	T21834 hypothetical prote
9	269.5	13.0	392	2	T45032 hypothetical prote
10	269	12.9	524	2	T23907 hypothetical prote
11	265	12.7	393	2	T25392 hypothetical prote
12	261.5	12.6	443	2	T21598 hypothetical prote
13	257.5	12.4	522	2	T24265 hypothetical prote
14	248.5	12.0	513	2	T28933 hypothetical prote
15	242.5	11.7	1910	2	H88124 protein t12c9.3 [i
16	242	11.6	643	2	T26616 hypothetical prote
17	240.5	11.6	325	2	T15584 potassium channel
18	240	11.5	461	2	T43394 potassium channel
19	239.5	11.5	452	2	T21118 hypothetical prote
20	236.5	11.4	427	2	T27681 hypothetical prote
21	232.5	11.2	307	2	H89074 protein twk-24 [im
22	231.5	11.1	539	2	T23700 hypothetical prote
23	230	11.1	1539	2	T30037 hypothetical prote
24	229	11.0	551	2	T16426 potassium channel
25	229	11.0	555	2	T43357 potassium channel
26	228	11.0	485	2	T24201 hypothetical prote
27	223	10.7	444	2	T26229 hypothetical prote
28	220	10.6	383	2	T23182 hypothetical prote
29	218.5	10.5	484	2	T43529 probable potassium

30	218.5	10.5	519	2	T16629 hypothetical prote
31	216.5	10.4	335	2	S44635 f22b7.7 protein -
32	213	10.2	475	2	T27725 hypothetical prote
33	211	10.1	769	2	T27550 hypothetical prote
34	210	10.1	631	2	T26232 hypothetical prote
35	205	9.9	544	2	T43364 potassium channel
36	205	9.9	576	2	T43363 potassium channel
37	204	9.8	550	2	T22557 hypothetical prote
38	202.5	9.7	1136	2	T26953 hypothetical prote
39	201	9.7	381	2	T43393 potassium channel
40	199	9.6	681	2	T19429 hypothetical prote
41	198	9.5	383	2	T23746 hypothetical prote
42	197.5	9.5	569	2	T43531 probable potassium
43	194	9.3	586	2	T21683 hypothetical prote
44	193.5	9.3	757	2	T24266 hypothetical prote
45	192	9.2	405	2	T21188 hypothetical prote

ALIGNMENTS

RESULT 1
S65566 inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65566
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanl
EMBO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove
A:Reference number: S65566; MUID:96183184
A:Accession: S65566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: EMBL:U03632; NID:q1086490; PIDN:AAB01688.1; PID:q1086491

Query Match 18.3%; Score 379.5; DB 2; Length 336;
Best local similarity 34.4%; Pred. No. 2.2e-17;
Matches 90; Conservative 54; Mismatches 95; Indels 23; Gaps 9;

QY 2 RSTLLALLLV-VLLYVSGALVFOALQEPHOQAKKMDHGDQFLRDHPVCSOKSLSD 60
DB 18 RSANCFEPLVGLVLYVFGAVFSSVELPYEDLLKRLKRRLEHECLSEQDLQ 77
QY 61 FIKLLVVALGCG---ANPETSWTNSSNHSANMLGSAFFSGTITTTIGYINVLHTDA 116
DB 78 FLGRVLEASNNGVSLNASGNMN-----MDFTSLFFASTVLTGTGHTVPLSDG 129
QY 117 GRLCIFRVALGIFLFGMLAGVADRGLSSL-RRGIGHIAIFLKMVRPPGLVRSAYL 175
DB 130 GKACLIIVSYIGIFPTLLFLTAAVQRTVHYTRPVLYFH---TRWFSQVVAIYAVL 186
QY 176 --FLICGLFVLAPTFVFSYME-SWSKLEAIYVITLTVFGDVPDGTGON--SPA 231
DB 187 LGFTVSCFFFI--PAAVFSLVEDDMNLFESFYCFISLISIGLDVVPDGGVQKREL 244
QY 232 YQPLVEMWILFGLAFASVLT 253
DB 245 YKIGITCYLLGLTAMLVLET 266

RESULT 2
potassium channel protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A:Title: OKR1, a potassium-selective leak channel with two pore domains cloned from D
A:Reference number: Z17770; MUID:97075152

[illegible]

RESULT	5
T32347	

RESULT	5
T32347	

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: J32347
R:Murray, J.; Wohlmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid F34D6.
A:Reference number: Z21153
A:Accession: J32347
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <MUR>
A:Cross-references: EMBL:AF025454; PIDN:ACG71151.1; GSPDB:GN00020; CESP:F34D6.3
A:Experimental source: strain Bristol N2; clone F34D6
C:Genetics:
A:Gene: twk-23; CESP:F34D6.3
A:Map position: 2
A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match	15.1%	Score 314.5;	DB 2;	Length 336;
Best Local Similarity	31.5%	Pred. No. 3.3e-13;		
Matches 94;	Conservative 43;	Mismatches 118;	Indels 43;	Gaps 9;

QY 7 LALLALVLLVLVS GALVFQALEOEHQQAKKMDHGDDQLRHPVCVSOK---SLED FIK 63
QY :
Db 9 LSLIVCTLTYYLVLGA AFDAL ETE NEIL QYRG LGEP RKLVQR VREKL KTYNMS NADY-- 66

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QY      64  LTVLEALGGANPETSMTNSSNNSSA -WNLGSAFFESFGITITTCGNCIVLHTDAGRFC 121
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      67  ---EIL-----EATIVKSVPHKAGYQKFGSAGYFATVITTTIGYGHSTPMTDAGKVC 117

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QY      122  IFVALGPIEGMLLGVDRGS-----SLRGIGIHFAIFLKNMHPGGLVRSLSAV 174
          : 111 111  : :11: : 11 1
Db      718  MLYALAGIPGLIMFOSIGERANTFAAKLLRFIRFAG-----KQPIVTSDDL 166

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Db 167 IFCGCGGLLIFGCAFMFSSYEKNTYPAVYYCEVTLTITIGFGDYALQKRGSLSQTPPEY 228

227 VEEFLVFLFGTLVISAAMLL--VLEFLTMNTEDERRDEGEAILLAAGLVRYSDPTA 2822

RESULT 6
T43361
probable potassium channel chain n2p20 - *Caenorhabditis elegans*

C:Accession: T43361
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000
C:text_change 11-Jan-2000
R:Wang, Z.W.; Salkoff, L.

A/Description: Potassium channels in *C. elegans*
A/Reference number: Z22450
A/Accession: T43361

A;Molecule type: mRNA
A;Residues: 1-364 <WAN>
A;Cross-references: EMBL:AF083646; PIDN:AAC32857.1

Query Match	14.4%	Score 298.5	DB 2	Length 364
Best Local Similarity	25.9%	Pred No. 3.8e-12		
Matches 103	Conservative 56	Mismatches 15	Totals 75	Cases 13

QY 2 RSTLLALLLVLYVSGALVFQALEQPHHQQAOKKMDHGRDQFLRDHPVCSOKSIEDF 61
 ::|||:|||||:::|||||:::|||||
 Db 7 KSARALLILITSTFYVILFGAMVFEDKLESEKDTWVRDQEFERTIDR-TLKHVNESESDILHLF 65

OY 62 IKLVEALGGANPETSWTNTSSNHSAMNLGSAFFFSGLTTITIGYGNIVLH7DAGRLEC 12

Db 66 EAIATISIPQAGYO-----WOFAGAFCEATVTVTTGVGSHASPSNAGKLEC 11

QY 122 IFYALVGIPLFGMLLAGVGDRLSSLR-----RGIGHIEAIFLKNHVPGLVRSLSAVL 175

Db	114	MIFALFGEVPMGLIMFQSGEVRNFEEFIATSLKHFDRSLHQOGEFTCLQETPTPHILMVS---	1707
Oy	176	FLILGCLLFVLTTPHFEVSYMESMSKLEAVIYVITLTITVVGGDVPPDDGNG--ONSBAQ	233
Db	171	LITG-FEVIYSGVMEFTTIKMSIFDVIYTCMTITFTSGDGLVPLQOANALDDQPLV	228
Oy	234	PLVWFILIEGLIYFASVLTITIGNMLRAVSRRTRAEMGGLTAQAASMTGVTARVTOETGP	293
Db	229	FATIMFIIIGLIVFASACVNL-----VLGFMSMDEVTYA--AOREPP	265
Oy	294	SAPPEK--EODPLPSSLPAPPAVAVEPAGRGSPAPAEKVEYTPSPATSLADPSENLAF	351
Db	270	SAIVERTSRNSLVDSQIFNIQKHSYGVLEGRPRMYSI-----VPNSTA-	315
Oy	352	IDESSDTOSER-----GCALPRAPRG-----RRP	376
Db	316	DVHLRRSTRSRISODIYVCCGCFKRPFRPHHFFSLTRR	352

RESULT 7

hypothetical protein C40C9.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: M10860

R;Hembry, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19860

A;Status::preliminary; translated from GR/EMBL/DBS
A;Molecule type: DNA
A;Residues: 1-334 <WIL>
A;Cross-references: EMBL:270266: PIDN:CA94204.1; G

A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X

Query Match 14.0%; Score 291.5; DB 2; Length 334;

QY 2 RSTTLLALLLVLLVSGALVEQALEQPHQQQAQKKMDHGRDQFLRDHPCVSQKSLDE 61
Matches 82; Conservative 59; Mismatches 116; Indels 45; Gaps 8;

Db 7 KSARALLILSTFTYLLFGAMVEDKLESEKDTWVDEIERITDR-LKHKYNESERDLHF 65

QY 62 IKLLVEALGGANPETSMTNSSNHNSSAMNLGSAFFESGTLITTYIGYNIVLHTDAGRLEC 121

Db 66 EAIAIKSIPQAGYQ-----WQFAGAFYFATVVTITVVGIGHSAPSTNAGKLEFC 113
QY 122 IFYALVGIPLEFGMLLAGYGDRLSSLR-----RGIGHIEAIFLKNHVPGLVRSLSAVL 175

Db 114 MFALEGVPMGLIMFQSIGERVNTFIATSLAKFRDSLHQGPTCLGEVTPTHLLMVS--- 176
Qy 176 FLIGCLLVLTPTFVESYMESSKLEAIYFVIWLTTFVGEGDYVPDGTG--QNSPAQ 233

Db 171 -LTIG-FMVIASGTYMEHTIEKNSIFDAYEFCMIHFSTIGDGLPLQGVNMLQDQPLVY 222

Qy 234 PLVWFMLFGIAYFASVLTITGNMLRAVSRRTRAEMGGLTAQASWITGTVTARVQTQTP 293

Db 229 FATIMILIGLAVSACVNL-----VLGFMASNADEVTA--AQREPP 265
QY 294 SA 295

DB	2/0	SA	2/1
RESULT 8			

hypothetical protein F36A2.4 - *Caenorhabditis elegans*


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QY 165 -----PGLVRSLS----- 172
Db 224 PNNNPVTAAATASAGGCTGRRKKOORDVSNAGTFNDINSEINDOSSEGENNEGEDEEQ 283
QY 173 -----AVFLILGCLLEFLTPTEVFSYMSWSKLAIFYVITLTGFGDIV 220
Db 284 IQPDSNHEKRVSVLFLILMLGVAAGAYIVMMEWTFEFAFYFCFVTTIGFDIV 343
QY 221 PGDGTGNSPAVOPPLVFWMLFLFLAFASVLTIGN-WLRNARSRRRA-----EMGGLT 273
Db 344 PA-----NDWMLPATLAYIVFGLITTCIDLVGSEYIRLDHFYGRSLGRQPMITGKV 397
QY 274 AQAASWTGTATARTORTGSPAPPEKEOPLPSSLP-----APPAVPEPAGRP 322
Db 398 VHLGEVGVY-AFLQKNGTLTA-----EQITKLSQLPBEYLIDCLINGQPDLMNMGSRP 451
QY 323 GSPAPA--EKVETPSPTASALDYSENIAFIDESSDTOSERGCLAPR-APR 371
Db 452 YVPPDIYFKWIEHP-----RTLSFASDRVLOSMSIDLNTSR-CSTARTLTPR 499

RESULT 11
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25392
R:Lloyd, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: 220027
A:Accession: T25392
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393 <MIL>
A:Cross-references: EMBL:Z92813; PIDN:CA807286.1; GSPDB:GN00021; CESP:T28A8.1
A:Experimental source: clone T28A8
C:Genetics:
A:Gene: CESP:T28A8.1
A:Map position: 3
A:Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match 12.7%; Score 265; DB 2; Length 393;
Best Local Similarity 24.8%; Pred. No. 5.8e-10;
Matches 77; Conservative 50; Mismatches 93; Indels 90; Gaps 8;

QY 7 LALLALVLYLVSGALVFOALEOP-----HEQQAQKKMDHGRDQFLRDHP 51
Db 15 VSLIVLSVYVVGAFILYQLEOPNEVVRANIERFNHKKROMLEHLEMRESIGQHV 74
QY 52 C--VSOKSLDEPFIKLVEALG-----GGANPETSWTSSNHNSSANNLGSAPFS 98
Db 75 VEDLAVKYVDNVTIRLFEAFDTHCIGAKHLRPGCEDEYDNTYM-----TALFFT 124
QY 99 GTITTTIGGNIVLHTDARLFCIFAYALGIPFLFGMLAGVDRGSSLR----- 149
Db 125 TLLTLTIGGNLPTVRGKRLCTIALFGVPLILTVADIKFLENTVOLTYRKLK 184
QY 150 -----GIGHIEAIFLKMHWPPGLVRSLSAVLFIILGCLFVL 186
Db 185 EKSKOKYVSISSKDKKNKEDNLMDHLE-----NYISIPFLIVAILLSYI 231
QY 187 T-PTFEVSYESWSKLEAIFYVLTITVGFQDYPGDDGTGNSPAVOPPLVFWMLFGIA 245
Db 232 TFGAVVLSMWEKWDFFSGFYSEITMTVTFGSDIV-----LKREYILDLCTIIGLS 285
QY 246 YFASVLTITIG 255
Db 286 ITTWCIDLVG 295

RESULT 12

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T21598
hypothetical protein F31D4.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21598
R:Mortimore, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: 219447
A:Accession: T21598
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-443 <MIL>
A:Cross-references: EMBL:Z92832; PIDN:CA807375.1; GSPDB:GN00023; CESP:F31D4.7
A:Experimental source: clone F31D4
C:Genetics:
A:Gene: CESP:F31D4.7
A:Map position: 5
A:Introns: 13/3; 90/2; 149/1; 222/3; 290/3

Query Match 12.6%; Score 261.5; DB 2; Length 443;
Best Local Similarity 27.5%; Pred. No. 1.1e-09;
Matches 84; Conservative 49; Mismatches 96; Indels 77; Gaps 10;

QY 9 LIALVLYLVSGALVFOALEOPHEQQAQ-----KKMDHGRDQFLRD 49
Db 17 LIIVFLIYCISGLVFWLIEEPYQSELRDAMQHKIENNRARVADAMMKIFNNSDYLIYI 76
QY 50 HPCVSOKSLDEPFIKLVEALGCGANP-ETSWTSSNHNSSANNLGSAPFSGTITITIGV 108
Db 77 KGMTSQRLTTFEFI-----ELGSYENQGVKW--SQKKMDMWNNAVLPAGTICTTITIG 129
QY 109 NIVLFTDAGRLFCIFAYALGIPFLFGMLLAGVDRGSSLRGIGHIEAIFLKMHWPPGLV 168
Db 130 HLPMTDGRMLTMTFALFGIPMLVLVQDGRKLLITMK-----FPWFQRRRLM 179
QY 169 RSLSAV-----LFLIGCLLVLPPTFPFSYM-----ESWS 199
Db 180 RRLMCCFTKQPIEMKEIEROBRHDLDFDLPLPVGIAL-LVTWIFLCSFVLSVMDHNM 238
QY 200 KLEAIFYVLTITVGFQDYPGDDGTGNSPAVOPPLVFWMLFGIAVFAVLTITIGNMLR 259
Db 239 LLESFFFTSLSTVGLGDLVP-----SSRLILTMGFLIVGL-----SLYSNVILIQ 288
QY 260 AVSRRT 265
Db 289 AKMKST 294

RESULT 13
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T24265
R:Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: 219866
A:Accession: T24265
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-522 <MIL>
A:Cross-references: EMBL:Z70036; PIDN:CA93875.1; GSPDB:GN00028; CESP:T01B4.1
A:Experimental source: clone T01B4
C:Genetics:
A:Gene: CESP:T01B4.1
A:Map position: X
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.4%; Score 257.5; DB 2; Length 522;
Best Local Similarity 26.1%; Pred. No. 2.4e-09;
Matches 79; Conservative 42; Mismatches 87; Indels 95; Gaps 10;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 4, 2002, 11:00:36 ; Search time 31.9 Seconds
(without alignments)
2158.369 Million cell updates/sec

Title: US-09-655-272-2
Perfect score: 2079
Sequence: 1 MRSTLLALALVLLVLSG.....SKKPSRPPGRLKDKANPV 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1692.5	81.4	419	4 Q96T94	Q96T94 homo sapien
2	969	46.6	186	11 Q925Q7	Q925Q7 rattus norv
3	776.5	41.1	4 Q9NRT2	Q9NRT2 homo sapien	Q9NRT2 homo sapien
4	768.5	37.0	370	11 Q92414	Q92414 rattus norv
5	768.5	37.0	426	11 Q920B6	Q920B6 rattus norv
6	495.5	23.8	309	4 Q96T55	Q96T55 homo sapien
7	490	23.6	294	4 Q9H591	Q9H591 homo sapien
8	433.5	20.9	343	4 Q9H591	Q9H591 homo sapien
9	428.5	20.6	332	4 Q96T54	Q96T54 homo sapien
10	421	20.3	502	11 Q9JK62	Q9JK62 mus musculu
11	415.5	20.0	241	11 Q9CX88	Q9CX88 mus musculu
12	390	18.8	313	11 Q9ERU5	Q9ERU5 rattus norv
13	376.5	18.1	336	11 Q92T22	Q92T22 rattus norv
14	370.5	17.8	229	11 Q9H592	Q9H592 homo sapien
15	365	17.6	259	6 Q92821	Q92821 oryctolagus

17	347.5	16.7	248	11 Q9DA02	Q9DA02 mus musculu
18	336.5	16.2	330	4 Q9HBC8	Q9HBC8 homo sapien
19	332.5	16.0	299	11 Q9OX34	Q9OX34 mus musculu
20	323	15.5	396	11 Q923V6	Q923V6 rattus norv
21	322.5	15.5	395	11 Q9JLD4	Q9JLD4 rattus norv
22	322	15.5	329	5 Q17185	Q17185 caenorhabdi
23	315.5	15.2	330	4 Q9H427	Q9H427 homo sapien
24	308.5	14.8	237	11 Q9ES08	Q9ES08 rattus norv
25	306.5	14.7	343	11 Q9J114	Q9J114 mus musculu
26	300	14.4	398	5 Q9YFS9	Q9YFS9 drosophila
27	298.5	14.4	364	5 Q9VHE0	Q9VHE0 caenorhabdi
28	298	14.3	340	5 Q9VHE0	Q9VHE0 drosophila
29	293	14.1	392	11 Q9ESM5	Q9ESM5 rattus norv
30	282	13.6	405	11 Q9ERS0	Q9ERS0 homo sapien
31	281	13.5	408	4 Q96E79	Q96E79 caenorhabdi
32	279	13.4	654	5 P90863	P90863 caenorhabdi
33	276	13.3	408	4 Q9HB14	Q9HB14 homo sapien
34	269.5	13.0	392	5 Q9NEV3	Q9NEV3 caenorhabdi
35	269.5	13.0	411	5 Q952J4	Q952J4 caenorhabdi
36	269	12.9	524	5 Q21729	Q21729 caenorhabdi
37	265	12.7	393	5 Q9XU07	Q9XU07 caenorhabdi
38	263	12.7	430	11 Q9ERS1	Q9ERS1 rattus norv
39	261.5	12.6	443	5 Q45422	Q45422 caenorhabdi
40	259.5	12.5	237	11 Q920G1	Q920G1 rattus norv
41	259.5	12.5	430	4 Q9HB15	Q9HB15 homo sapien
42	257.5	12.4	522	5 Q22042	Q22042 caenorhabdi
43	257	12.4	395	5 Q9V362	Q9V362 drosophila
44	256	12.3	385	5 Q9VY55	Q9VY55 drosophila
45	248.5	12.0	513	5 Q22940	Q22940 caenorhabdi

ALIGNMENTS

RESULT	ID	Q96T94	PRELIMINARY;	PRT:	419 AA.
AC	Q96T94	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	TWO PORE K+ CHANNEL KT4.1B.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Ozaita A., Vega-Saenz de Miera E.C.;				
RT	"Cloning of Two transcripts of the Human 2-pore K+ channel KT4.1 Gene.				
RT	Chromosomal Localization, Tissue Distribution and Functional				
RT	Expression."				
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF259501; AAK49390.1; -				
KW	Ionic channel.				
SQ	SEQUENCE 419 AA; 45173 MW; E7DEDE17B30CFBF CRC64;				

Query Match	81.4%; Score 1692.5; DB 4; Length 419;
Best Local Similarity	82.4%; Pred. No. 1.4e-117;
Matches 328; Conservative	24; Mismatches 41; Indels 5; Gaps 2;
QY	1 MRSTLLALALVLLVLSGALVFOALQPHQQAQKMDHGRQFLDHCVCYSQSLSD 60
DB	27 MRSTLLALALVLLVLSGALVFOALQPHQQAQKMDHGRQFLDHCVCYSQSLSD 86
QY	61 FKLLVEALVGGAGNPETSWNSNNSAMNGSAFFSGTITTTGYGNIVLHDTAGRLF 120
DB	87 LIKEVADALVGGAGNPETSWNSNNSAMNGSAFFSGTITTTGYGNIVLHDTAGRLF 145
QY	121 CIFYALVGIPLFGMLAGVGRGLSSLRGIGIHAIPLKWHVPPGLYRSAYVFLILG 180
DB	146 CIFYALVGIPLFGMLAGVGRGLSSLRGIGIHAIPLKWHVPPGLYRSAYVFLILG 205

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QY 181 CLLEVLPTPEFVSYSMSKLEAIFYVITLTVGFQDYPVPGDGTGONSPAYOPLVWFI 240
DB 206 CLLEVLPTPEFVSYSMSKLEAIFYVITLTVGFQDYPVPGDGTGONSPAYOPLVWFI 265
QY 241 LFGALAFASVLTITIGMWLRAVSRRTAEMGGLTAQAASWTGVTAVTORTGSPAPPEK 300
DB 266 LGLAFASVLTITIGMWLRAVSRRTAEMGGLTAQAASWTGVTAVTORTGSPAPPEK 325
QY 301 EGPLPSSLPAPAVPEPAGRPSPPAPKVEPSPPTASALDYPSENAFIDESSDTOS 360
DB 326 EGPLPSSLPAPAVPEPAGRPSPPAPKVEPSPPTASALDYPSENAFIDESSDTOS 381
QY 361 ERGCALPAPRCRRRPNPKSPRPGRLDKAPV 398
DB 382 ERGCALPAPRCRRRPNPKSPRPGRLDKAPV 419

RESULT 2
Q92507 PRELIMINARY; PRT; 186 AA.
AC Q92507;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TWO PORE K+ CHANNEL KT4.1 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Ozata A., Vega-Saenz de Miera E.C.;
RT "Cloning of two transcripts of the Human 2-Pore K+ channel KT4.1 Gene.
RT Chromosomal Localization, Tissue Distribution and Functional
RT Suppression."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF259502; AAK49391.1;
KW Ionic channel.
FT NON-TER
SO SEQUENCE 186 AA; 19828 MW; AB07DAD8C867FEC7 CRC64;

Query Match 46.6%; Score 969; DB 11; Length 186;
Best Local Similarity 98.4%; Pred. No. 2; Le-64;
Matches 182; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 214 VGFQDYPVPGDGTGONSPAYOPLVWFIIFGLAFASVLTITIGMWLRAVSRRTAEMGGLT 273
DB 2 VGFQDYPVPGDGTGONSPAYOPLVWFIIFGLAFASVLTITIGMWLRAVSRRTAEMGGLT 61
QY 274 AQAASWTGVTAVTORTGSPAPPEKEQPLPSSLPAPAVPEPAGRPSPPAPAEKVEET 333
DB 62 AQAASWTGVTAVTORTGSPAPPEKEQPLPSSLPAPAVPEPAGRPSPPAPAEKVEET 121
QY 334 PSPPTASALDYPSENAFIDESSDTOSERGCALPAPRCRRRPNPKSPRPGRLDKAPV 393
DB 122 PSPPTASALDYPSENAFIDESSDTOSERGCALPAPRCRRRPNPKSPRPGRLDKAPV 181
QY 394 KAVPV 398
DB 182 KAVPV 186

RESULT 3
Q9NRT2 PRELIMINARY; PRT; 411 AA.
AC Q9NRT2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.

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GN TREK-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN.
RX MEDLINE=20244931; PubMed=10784345;
RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
RA Medhurst A.D., Murdoch P., Chapman C.G.;
RT "Cloning, localisation and functional expression of the human
RT orthologue of the TREK-1 potassium channel."
RL Pfluegers Arch. 439:714-722(2000).
DR EMBL: AF171068; AAF89743.1;
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001622; Channel_pore_K.
DR pfam: PF003976; Trek_channel.
DR pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01499; TREKCHANNEL.
KW Ionic channel.
SO SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;

Query Match 37.3%; Score 776.5; DB 4; Length 411;
Best Local Similarity 49.8%; Pred. No. 9; Se-50;
Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;

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QY 1 MRSTTLALALVALYVSAFQALFOLEPHQOAKKMDHGDOPLRHPCYSQKSLSD 60
DB 42 MKKKTIVTIVLVYLIITATVFAKLEOPHEISQRTTVIQOTFISQHSVCNSTEIDE 101
QY 61 FIKLVEALGAGANPETSMTNSNHSANLGSAPFFSGTITITIGYGNIVLHTDAGRLE 120
DB 102 LIQOIVAAINAGILP--LGNTSNOISHWDLGSSFFACVITITIGFNGISPRTEGKIF 158
QY 121 CIFVALVGIPLFGMLAGVDRGLSGIRGIGIEAIFLKNHVPOLVSLAVLEFLIG 180
DB 159 CIYALIGIPLEFGLAGDGLTIFGKINAVEPTFKMWSQTKRIITITIFILFG 218
QY 181 CLLEVLPTPEFVSYSMSKLEAIFYVITLTVGFQDYPVPGDGTGONSPAYOPLVWFI 240
DB 219 CVLVALPALIFKHIGWSALDAIVFVITITIGDGVYAGSDIEYDFKPYVWFI 278
QY 241 LFGALAFASVLTITIGMWLRAVSRRTAEMGGLTAQAASWTGVTAVT 285
DB 279 LVGLAFASVLTITIGMWLRAVSRRTAEMGGLTAQAASWTGVTAVT 323

RESULT 4
Q92414 PRELIMINARY; PRT; 370 AA.
AC Q92414;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE MECHANOSENSITIVE TANDEM PORE POTASSIUM CHANNEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=21268449; PubMed=11374070;
RA Kim Y., Bang H., Gattenco C., Kim D.;
RT "Synergistic interaction and the role of C-terminus in the activation
RT of TRAAK K+ channels by pressure, free fatty acids and alkali."
RL Pfluegers Arch. 442:64-72(2001).
DR EMBL: AF302842; AAK60504.1;
KW Ionic channel.

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RP SEQUENCE FROM N.A.
 RA Williams S.
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL136087; CAC07336.1;
 DR InterPro: IPR003280; 2porek_channel.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR Pfam: PF00520; Ion_trans_1.
 DR PRINTS: PR01333; 2PORECHANEL.
 KW Ionic channel.
 SQ SEQUENCE 294 AA; 32507 MW; FCBA3B352F1F0952 CRC64;

Query Match 23.6%; Score 490; DB 4; Length 294;
 Best Local Similarity 40.8%; Pred. No. 1,1e-28;
 Matches 102; Conservative 54; Mismatches 78; Indels 16; Gaps 5;

DB 6 LIALALVLLVLYSGALVFAQLPHEQQAOKKMDGRDQFLRDHPVCSKSLDEDTKL 65
 14 VLPLLVAVCYLLGATIFOLLERQAEQSRDQFLEKLFLENYICLDQMAEQFQVY 73
 QY 66 VEALGGANPETSWTNSNNSAMNLSAFPEFGTITTTGIGNIVLHTDAGRLFCIFYA 125
 DB 74 MEAWKGVNPRGNSTNSN-----WDESSSEFAGTAVTTIGYGNLAPSTEAGQVCFVYA 129
 QY 126 LVGIPLEGMILAGVGRDLGSSLRGIGITEAIFLKWHPV---GLVRSLSAVLFLIGCL 182
 DB 130 LGLIPLVIFL---NHLGTGLRAHLAIE---RREDPRRSQVLYQVIGLALFTLTGL 181
 QY 183 LFTVTFEVSMESSKLEAIFVIVTLTVGFGDYVPG-DGTGONSAPVQPLVFWML 241
 DB 182 VILFPPMVSHEGWSFSEGFYFAFITLSTVGFGDYVGTDPKSHYISVRSLSAIVIL 241
 QY 242 FGLAFVPSVLT 251
 DB 242 LGLAMLALIL 251

RESULT 8
 Q9BXDI PRELIMINARY; PRT; 343 AA.
 AC Q9BXDI;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADRENAL GLAND;
 RX MEDLINE=21145510; PubMed=11248242;
 RA Decher N., Maier M., Dittlich W., Gassenhuber J., Bruggemann A.,
 RA Busch A.E., Steimeyer K.;
 RT "Characterization of TASK-4, a novel member of the pH-sensitive, two-
 pore domain potassium channel family.";
 RL FEBS Lett. 492:84-89(2001).
 DR EMBL: AF39912; AAK28551.1;
 DR InterPro: IPR003280; 2porek_channel.
 DR InterPro: IPR000636; Cation_chan_non_lig.
 DR Pfam: PF00520; Ion_trans_1.
 DR PRINTS: PR01333; 2PORECHANEL.
 SQ SEQUENCE 343 AA; 38172 MW; 29B1F354CE22E3BB CRC64;

Query Match 20.9%; Score 433.5; DB 4; Length 343;
 Best Local Similarity 36.2%; Pred. No. 1.9e-24;
 Matches 111; Conservative 49; Mismatches 120; Indels 27; Gaps 7;

DB 22 TVLLLA-LVIALGTGVFTLEGRAQDSSRSRQNRKWEILNFTCLDRPALDSLIRD 80
 QY 65 LVEALGGANPETSWTNSNNSAMNLSAFPEFGTITTTGIGNIVLHTDAGRLFCIFY 124
 DB 81 VQAKAKNGA-----SLNSTSMGRWELVGSFFSVSTTTIGYGNLSPNTMAARLFCIF 136
 QY 125 ALVGPLEGMILAGVGRDLGSSLRGIGITEAIFLKWHPVGLVRSLSAVLFLIGCLF 184
 DB 137 ALVGIPLVLYL---NRLGHLMOQGVNHNASRLGTTWOPDARKWLASGALLSGLLF 192
 QY 185 VTFEVSMESSKLEAIFVIVTLTVGFGDYVPGDGTGONSAP-YQPLVFWILFG 243
 DB 193 LILPPLLESHMEGWSYEGFYFAFITLSTVGFGDYVGNMPSQRYPLWKKNVSLMILFG 252
 QY 244 LAYFASVLTITGNMLRAVSRT---RAEMGGLAQASWTGVTVARVQR--TGPSADP 297
 DB 253 MA-----WLAISNSSSPSMRQGGYPAATYTLRKTSSPRAGDRDLTGSSQPT 301
 QY 298 PEKQPL 304
 DB 302 PHSKDAI 308

RESULT 9
 Q96T54 PRELIMINARY; PRT; 332 AA.
 ID Q96T54;
 AC Q96T54;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 2P DOMAIN POTASSIUM CHANNEL TALK-2.
 GN CNK17.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
 RA Lazdunski M., Lesage F.;
 RT "Genomic and functional characteristics of novel human pancreatic 2P
 RT domain K⁺ channels.";
 RL Biochem. Biophys. Res. Commun. 0:0-0(2001).
 DR EMBL: AF358910; AAK49533.1;
 KW Ionic channel.
 SQ SEQUENCE 332 AA; 36894 MW; 1848DBC06E078158 CRC64;

Query Match 20.6%; Score 428.5; DB 4; Length 332;
 Best Local Similarity 36.0%; Pred. No. 4.4e-24;
 Matches 111; Conservative 49; Mismatches 115; Indels 33; Gaps 8;

QY 4 TTLALALVLLVLYSGALVFAQLPHEQQAOKKMDGRDQFLRDHPVCSKSLDEDTKL 63
 DB 21 STVLLLA-LVIALGTGVFTLEGRAQDSSRSRQNRKWEILNFTCLDRPALDSLIR 79
 QY 64 LVEALGGANPETSWTNSNNSAMNLSAFPEFGTITTTGIGNIVLHTDAGRLFCIF 123
 DB 80 DVQAYKNGA-----SLNSTSMGRWELVGSFFSVSTTTIGYGNLSPNTMAARLFCIF 135
 QY 124 YALVGPLEGMILAGVGRDLGSSLRGIGITEAIFLKWHPVGLVRSLSAVLFLIGCLF 183
 DB 136 FALVGIPLVLYL---NRLGHLMOQGVNHNASRLGTTWOPDARKWLASGALLSGLLF 191
 QY 184 VTFEVSMESSKLEAIFVIVTLTVGFGDYVPGDGTGONSAP-YQPLVFWILF 242
 DB 192 LILPPLLESHMEGWSYEGFYFAFITLSTVGFGDYVGNMPSQRYPLWKKNVSLMILF 251
 QY 243 GLAFVPSVLTITGNMLRAVSRT---RFAEMGGLAQASWTGVTVARVQRGTGPSA 295
 DB 252 GMAWMLALITKLISOLETPGRVCSCHHSKEDP-----KSGSR-----RQGPDR 296

QY	296	PPREKOP	303
Db	297	-EPESHSP	303
RESULT	10		
ID	09JK62	PRELIMINARY;	PRT: 502 AA.
AC	09JK62:		
DT	01-OCT-2000	(TREMBLrel. 15, Created)	
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)	
DE	POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).		
GN	CKNK5.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129/SVJ; TISSUE=KIDNEY;		
RA	Roux J., Barhanin J.;		
RT	"Mouse two P domain potassium channel TASK2.";		
RL	Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		
RA	Cid L.P., Niemeyer M.I., Sepulveda F.V.;		
RT	"Functional properties of mouse TASK-2 potassium channel.";		
RL	Submitted (Nov-2000) to the EMBL/Genbank/DBJ databases.		
RN	EMBL: AF258395; AAF6868.1;		
DR	EMBL: AF319542; AAG3065.1;		
DR	MGD: MGI:136175; Kcnk5.		
DR	InterPro: IPR003280; 2porek_channel.		
DR	InterPro: IPR00636; Cation_chan_non_1fg.		
DR	InterPro: IPR001622; Channel_pore_K.		
DR	Pfam: PF00520; Ion_trans.1.		
DR	PRINTS; PRO1333; 2PORECHANNEL.		
KW	Ionic channel.		
QO	SEQUENCE 502 AA; 55976 MW; E4CE7/CC71B44D95 CRC64;		
Query Match	20.3%;	Score 421; DB 11; Length 502;	
Best Local Similarity	26.8%;	Pred. No. 2, 6e-23;	
Matches 129; Conservative	70; Mismatches 147; Indels 136; Gaps		
QY	9	LIALVLIVYSGALVFOALEQPHEDQAKMDHGRDOFLRDNHCYVQKSLDFIKILVER	68
DB	8	LTSALIFYLALGAILEVELEPEHPMKKKNVYQKHLKLEFCLQDEGLDKLLQVVSDA	67
QY	69	LGGSANETSWTUNSSNNSSAMNLSGAFSEFSGTITITIGYGNIVLHNDAGRLFCIFALV	128
DB	68	ADGVAVITGQTFNN-WNNPNMIFALYITITIGYGNVAPKPIAGHLFCVFGGLFG	122
QY	129	IPL-----FGMLDAGVGRDLGSSL-RRGIG-----HIEALFLKWHVPPGLVRLSLAV	174
DB	123	VPLCLTWISALGKRFGRARLGLFLRRGVSLRKAQITCTALFIYV-----	169
QY	175	LFLILGCLLVLPFTFFPFSIMESKKEIALIYVITLITVGGFGDYVPGDGTGQNSPA-YQ	233
DB	170	-----GLVLMHVLIPPFVFMTEEMNYIEGLYFSITITISTIGFGDFVAGVNPASANTHALYR	224
QY	234	PLVFWLILFGLAAYPASVYLTITGNML-----FAVSRRTR-----AEMG	270
DB	225	YFVELMITYGLAW-----LSLFWNNKVMFVYVHKAIKRRRRRKRESFESSPHSRKALQMA	280
QY	271	GLVA-----QAASWTGTV-----TARTYQRTGSPAP-----PREKEQPLLR	306
DB	281	GSTASKADVNIFFSLKKEETYNDLIKOIGKKAMMTSGGGERVPPPGHGLGPGQDRPLPTIP	340
QY	307	SLSLAP-----PAVVE-----PAG-RPGSPADAEVET-----	333
DB	341	ASL-APLVVYSKNNRPSSLEEVYSQLKKNGHVSRLGEGAGAGQANRKDSVQTSFEVFINQDNR	399

[illegible]

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RESULT 12
Q9ERU5 PRELIMINARY; PRT; 313 AA.
ID Q9ERU5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, last annotation update)
DE 2P DOMAIN K+ CHANNEL, TWIK-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RC MEDLINE=20435832; PubMed=10887187;
RA Patel A.J., Malingret F., Magnone V., Fosset M., Lazdunski M.,
RA Honore E., an inactivating 2P domain K+ channel.*;
RT "TWIK-2, an inactivating 2P domain K+ channel.*";
RL J. Biol. Chem. 275:28722-28730(2000).
DR EMBL; AF281304; AAG10508.1; -.
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001622; Channel_pore_K.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01096; TWIK1CHANNEL.
DR Ionic channel.
SQ SEQUENCE 313 AA; 34214 MW; A93629568785CDBF CRC64;

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Query Match 18.8%; Score 390; DB 11; Length 313;
Best Local Similarity 35.1%; Pred. No. 2.9e-21;
Matches 98; Conservative 50; Mismatches 101; Indels 30; Gaps 8;

QY 8 ALLATVLT-----YLVSGALVFQALPOPEHQOAKKMDGRDQFLRDHCVCYSOKSLIEDFIK 63
DB 5 ALLASALVAVAGYGLGALLVARLERPHEARLRAELGLTRQDLNHSQCAVAHMLDAVE 64
QY 64 LIVERA-----LGGGANPETSMTNSSNHSAMNIGSAFFSGITITITIGYGNIVLHTDA 116
DB 65 RYLAAGRLGRAVLANASGP-----ANASD--PAMDFASALFFASLIVTMTGIGYTTPLTDA 118
QY 117 GRLECFYALVGIPLFGMLLAGVGDRLGSSLRIGIHAIFLKWHPVPGGLVRSLSAVLF 176
DB 119 GKASIVYALIGVPTMLLTLASAQRL--SLTLTHAPLSWLSLRWGMHPQFARAHMLVAL 176
QY 177 LLIGCLFVLPTTFVFSYM-ESMSKLEAIYFVITLTFVGFGDVPDGTGQ-NSPAYOP 234
DB 177 LMVIAIFPFLIPAAVFAVLEAWGFLEAFYFCFISLSTIGLGDVYVDEAPQPYRSLYKV 236
QY 235 LVMFMILFGLAYFASVLTITGNMLRAVSRRTAFEMGILT 273
DB 237 LVTAIFLGLVAVLVLOTF-----RRVSDLHGLT 266

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RESULT 13
Q922T2 PRELIMINARY; PRT; 336 AA.
ID Q922T2;
AC Q922T2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, last annotation update)
DE PUTATIVE POTASSIUM CHANNEL TWIK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,

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RA Kaczmarek L.K.;
RT "Cloning and localization of rTWIK, a putative potassium channel with
RT two P domains.*";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022819; AAD09336.1; -.
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01096; TWIK1CHANNEL.
DR Ionic channel.
RW SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;

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Query Match 18.1%; Score 376.5; DB 11; Length 336;
Best Local Similarity 34.4%; Pred. No. 3.2e-20;
Matches 90; Conservative 53; Mismatches 96; Indels 23; Gaps 9;

QY 2 RSTLLALAL-VLLYVSGALVFQALPOPEHQOAKKMDGRDQFLRDHCVCYSOKSLIED 60
DB 18 RSAMCFGLVLYGLLYLVFGAVVFSVELPYEDLLRQLKRLRFLHEHCLSEPOLBQ 77
QY 61 FIKLLVLEALGGG----ANPETSMTNSSNHSAMNIGSAFFSGITITITIGYGNIVLHTDA 116
DB 78 FLGVLERSNYSVLSMASGMN-----WDFTSALFFASTVLTGCGHTVPLSDG 129
QY 117 GRLECFYALVGIPLFGMLLAGVGDRLGSSLRIGIHAIFLKWHPVPGGLVRSLSAVLF 175
DB 130 GKAFCIIVSYIGIFLTLFVAVQRTVAVTRRPVLYER---IRNGFSQVAYAIYHAYL 186
QY 176 --FLIGCLFVLPTTFVFSYM-ESMSKLEAIYFVITLTFVGFGDVPDGTGQ-SPA 231
DB 187 LGFVTVSCFFPL--PAAVFSVLEDDNMFLSFYFCFISLSTIGLGDVYVDEAPQPYRSL 244
QY 232 YQPLVFMILFGLAYFASVLT 253
DB 245 YKIGITCYLLGLLMLVLET 266

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RESULT 14
Q99L99 PRELIMINARY; PRT; 336 AA.
ID Q99L99;
AC Q99L99;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 1.
GN KCKN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003729; AA03729.1; -.
DR MGD; MGI:109322; Kcnk1.
DR InterPro: IPR003280; 2porek_channel.
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01096; TWIK1CHANNEL.
RW SEQUENCE 336 AA; 38201 MW; 76B7FD5361A6216C CRC64;

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Query Match 18.1%; Score 376.5; DB 11; Length 336;
Best Local Similarity 34.4%; Pred. No. 3.2e-20;
Matches 90; Conservative 53; Mismatches 96; Indels 23; Gaps 9;

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QY      2 RSTLLALLAL-VLLYIVSGALVFOALEOPHEQOAKKMDGRDQFLRDHPVCSQKSLD 60
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      18 RSANCFGLVGLYLLIVFGAVSVSELPEDLLROELRKRLRFLHEECUSEPOLEQ 77
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61 FIKLLVEALGGG---ANPETSWTSSNHSAMNLSAFFPSGTTITIGYGNIVLHTDA 116
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      78 FLGRVLEASNYGVSIVLSNAGNMN-----WDFTSALFFASVLSLTIGYGHVPLSDG 129
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      117 GRLCIFPALVGIPLFGMLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPGVRSLSAVL 175
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      130 GKACCLISYVIGIPETLLFLAVAVQRYVTRRPLVYFH---IRMGFSKQVAIVHAVL 186
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      176 --FILIGCLFVLPPTVFSYME-SWSKLEAIVFVITVTVSGFDYVPGDGTGN-SPA 231
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      187 LGFTVYSCFFFI--PAVFSVLEDDMNFLSFYCFISLSTIGLGDYVPGGYNQKREL 244
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      232 YQPLVWFMLFGLAVFASVLT 253
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      245 YKIGITCYLLGLIAMLVLET 266
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 15

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Q9H592      PRELIMINARY;      PRT;      229 AA.
ID 09H592;
AC 09H592;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE D0137F1.1 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K )
DE (FRAGMENT).
DE D0137F1.1.
GN D0137F1.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136087; CAC07335.1; -
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR001622; Channel_pore_K.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel.
FT NON_TER      229
SQ SEQUENCE      229 AA;      25344 MW;      7AB9FB847E242ECE CRC64;

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Query Match 17.8%; Score 370.5; DB 4; Length 229;
 Best Local Similarity 40.6%; Pred. No. 5.6e-20;
 Matches 88; Conservative 37; Mismatches 83; Indels 9; Gaps 3;

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QY      4 TTTLLALLLVLYVSGALVFOALEOPHEQOAKKMDGRDQFLRDHPVCSQKSLD 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      21 STVLLILA-VIAYLALGTGFWTLGFGRAQDSSRSFQDKWELLQNTCLDRPALDSLIR 79
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      64 LLYEALGGGANPETSWTSSNHSAMNLSAFFPSGTTITIGYGNIVLHTDAGRLECF 123
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      80 DVOQAVYNGA---SLSNSTSMGRWELVGSFFSVSTITIGYGNLSPTMAARLCIF 135
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      124 YALVGIPLFGMLAGVGDRLGSSLRRGIGHIEAIFLKWHVPGVRSLSAVLFLIGCL 183
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      136 FALVGIPLNLVYL---NRLGHLMOQCVNHWASRLGCTWQDPKARLWAGSGLLSGLL 191
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      184 FVLPTFVFSYMSWSKLEAIVFVITVTVSGFDYV 220
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 FLILPPLFLSHMBGWSYEGFYFAFITLSTVGGDYV 228
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: June 4, 2002, 11:04:19
 Job time: 223 sec

